

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2006, 23:29:06 ; Search time 837 Seconds
(without alignments)
10995.661 Million cell updates/sec

Title: US-10-521-428A-1

Perfect score: 1320
Sequence: 1 atgaagtcgattcctagatgg.....cgtctgccagagctctgtga 1320

Scoring table: IDENTITY_NUC

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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1:  N_genseqeq_8:*
2:  1:  genseqeq19808:*
3:  2:  genseqeq19908:*
4:  3:  genseqeq20008:*
5:  4:  genseqeq20018a:*
6:  5:  genseqeq20018b:*
7:  6:  genseqeq20028a:*
8:  7:  genseqeq20028b:*
9:  8:  genseqeq20038a:*
10: 9:  genseqeq20038b:*
11: 10: genseqeq20038c:*
12: 11: genseqeq20038d:*
13: 12: genseqeq20048a:*
14: 13: genseqeq20048b:*
15: 14: genseqeq2005a:*
16: 15: genseqeq2006a:*

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SUMMARIES

Result	No.	Score	Query	Match	length	DB	ID	Description
	1	1320	100.0		1230	12	ADM82793	Adm82793 Human CB1
	2	1259.4	95.4		5665	10	ADL15026	Adl15026 Human CB1
	3	1259.4	95.4		5665	15	ASEE18784	Asee18784 Human CB1
	4	1257.8	95.3		1419	12	ACH91680	Ach91680 Human CB1
	5	1257.8	95.3		1507	2	AAO14003	Aao14003 Human CB1
	6	1257.8	95.3		1755	8	ABZ42646	Abz42646 Human can
	7	1257.8	95.3		1755	11	ADN38917	Adn38917 Cancer/ana
	8	1257.8	95.3		5471	13	ACN38515	Acn38515 Tumour-as
	9	1257.8	95.3		5460	14	AEA81160	Aea81160 Human can
	10	1257.8	95.3		5653	9	ADA24536	Ada24536 Human can
	11	1256.2	95.2		1419	12	ADH77050	Adh77050 hCB-1 dou
	12	1256.2	95.2		1419	12	ADH77050	Adh77050 hCB-1 dou
	13	1256.2	95.2		1419	12	ADO29849	Ado29849 Human GPC
	14	1256.2	95.2		2135	6	ABZ35604	Abz35604 Human gen
	15	1256.2	95.2		2135	10	ACA56852	Aca56852 Human sig
	16	1256.2	95.2		2135	10	ACC72645	Acc72645 Human can
	17	1256.2	95.2		2135	11	AD132143	Ad132143 Human CDN
	18	1256.2	95.2		2135	12	AD156648	Ad156648 Human pol1

15	Ad5842210	Human	lyw
16	Ab235298	Human	gen
17	Ab197974	Not-entog	
18	Adh77051	hCB-1-D38	
19	Adh18919	Cancer/an	
20	ABK34744	Human	CDN
21	Adn38921	Cancer/an	
22	Adn8116	Human	can
23	Adn82909	Ligand up	
24	Ado30140	Mouse	GPO
25	Ab199249	Mouse	isc
26	Aee11326	Hamster	c
27	Aee14968	Hamster	S
28	Ach77995	Human	gen
29	Ad172354	CB2R	gene
30	Ado30141	Mouse	GPO
31	Adq97952	Mouse	can
32	Adq97951	Mouse	can
33	Adq97955	Human	can
34	Adq97954	Human	can
35	Aee18785	Human	CB2
36	Ado29850	Human	GPO
37	Adva3394	Human	pay
38	Ab242647	Human	can
39	Aaq77797	Carnabino	
40	Acas6761	Human	sig
41	Ad132072	Human	CDN

ALIGNMENTS

XX	RESULT 1
XX	ADM82793
XX	ADM82793 standard; cDNA, 1320 BP.
XX	
AC	ADM82793;
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	Human cannabinoid 1 receptor splice variant CB1b-encoding cDNA.
XX	
KW	Human, CB1b receptor; splice variant; cannabinoid 1 receptor;
KW	CB1 receptor; drug screening; cannabinoid receptor-associated disorder;
KW	obesity; pain; psychiatric disorder; depression; anxiety;
KW	neurological disorder; Parkinson's disease; Alzheimer's disease;
KW	anorectic; analgesic; neuroleptic; antidepressant; tranquiliser;
KW	antiparkinsonian; neuroprotective; nootropic; gene therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	1..1320
FT	/*tag= a
FT	/product= "CB1b receptor"
XX	
PN	MO2004007551-A1.
XX	
PD	22-JAN-2004.
XX	
PE	14-JUL-2003; 2003WO-GB003067.
XX	
RR	17-JUL-2002; 2002SB-00002240.
XX	
PA	(ASTR) ASTRAZENCA AB.
PA	(ASTR) ASTRAZENCA UK LTD.
XX	
PI	Vu HK, Groblewski T, Greasley P;
XX	
DR	WPI: 2004-122892/12.
DR	P-PSDB; ADM82794.
XX	
XT	New human cannabinoid (CB) 1b receptor polypeptides and nucleic acid

PT molecules, useful for diagnosing, preventing or treating CB-associated
PT disorders e.g. obesity, pain, anxiety or neurological disorders and in
PT drug screening.

XX Claim 1; SEQ ID NO 1; 34pp; English.

CC The invention relates to a novel splice variant, CB1b (ADM82794), of the
CC human cannabinoid 1 (CB1) receptor and nucleic acids encoding it;
CC (ADM82793). Compared with the known CB1 receptor, the CB1b receptor has a
CC deletion of 33 residues towards the N-terminus (residues 22-54 of the CB1
CC receptor). The invention also relates to sequences at least 95% identical
CC to the CB1b receptor nucleic acid and protein sequences of the invention;
CC vectors and host cells comprising a CB1b receptor nucleic acid sequence;
CC a method for the recombinant production of the CB1b receptor; a method of
CC detecting a CB1b receptor nucleic acid; methods of screening or
CC identifying compounds which bind to the CB1b receptor; CB1b receptor
CC agonists, antagonists, inverse agonists or modulators and pharmaceutical
CC compositions containing them; and methods of treating or preventing a
CC disorder associated with cannabinoid receptors. The pharmaceutical
CC compositions and methods of the invention are useful in diagnosing,
CC preventing or treating CB receptor-associated disorders such as obesity,
CC pain, psychiatric disorders (e.g., depression or anxiety) or neurological
CC disorders (e.g., Parkinson's disease or Alzheimer's disease). The present
CC sequence represents cDNA encoding the human CB1b receptor.

XX Sequence 1320 BP; 291 A; 386 C; 335 G; 308 T; 0 U; 0 Other;

Query Match 100.0%; Score 1320; DB 12; Length 1320;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAAGTGGATCCTGATGAGCCTTGACAGATACACCTTCCGACATCAGCATGACCTC 60
DB 1 ATGAAGTGGATCCTGATGAGCCTTGACAGATACACCTTCCGACATCAGCATGACCTC 60
QY 61 CTGGAGAGTCCCTTCCAGAGAGATGACTGCGGAGACAAACCCAGCTAGTCTCCAG 120
DB 61 CTGGAGAGTCCCTTCCAGAGAGATGACTGCGGAGACAAACCCAGCTAGTCTCCAG 120
QY 121 GACCGAGTGAACATTACAGAAATTTTACAAAGTCTCTCTCTCTTCAAGAGATGAG 180
DB 121 GACCGAGTGAACATTACAGAAATTTTACAAAGTCTCTCTCTCTTCAAGAGATGAG 180
QY 181 GAGAACATCCAGTGGGAGAACTTCATGACATAGAGTGTTCATAGTCTCTGAACCC 240
DB 181 GAGAACATCCAGTGGGAGAACTTCATGACATAGAGTGTTCATAGTCTCTGAACCC 240
QY 241 AGCCAGAGCTGGCATTGCACTGCTCTCCCTCAAGCTGGGACCTTCAAGCTCTGAG 300
DB 241 AGCCAGAGCTGGCATTGCACTGCTCTCCCTCAAGCTGGGACCTTCAAGCTCTGAG 300
QY 301 AACCTCTGCTGCTGCTGCTCATCTCCACTCCGCAAGCTCTCCGTGACAGGCTTCTAC 360
DB 301 AACCTCTGCTGCTGCTGCTCATCTCCACTCCGCAAGCTCTCCGTGACAGGCTTCTAC 360
QY 361 CACTTCATCGGAGCGCTGGCGGTGGAGACCTCTGGGGAGTGTATTTTGTCTACAGC 420
DB 361 CACTTCATCGGAGCGCTGGCGGTGGAGACCTCTGGGGAGTGTATTTTGTCTACAGC 420
QY 421 TTCAATTGACTTCCACGCTGTTTCCACGCAAGATAGCCGCAAGTGTCTGTTCAAAC 480
DB 421 TTCAATTGACTTCCACGCTGTTTCCACGCAAGATAGCCGCAAGTGTCTGTTCAAAC 480
QY 481 GGTGGGGTCAAGGCTCTCTTCACTGCTCTCGTGGGAGGCTGTTCTCAAGCATGAC 540
DB 481 GGTGGGGTCAAGGCTCTCTTCACTGCTCTCGTGGGAGGCTGTTCTCAAGCATGAC 540
QY 541 AGGTACATATCATTCACAGGCGCCCTGAGCTTAAAGAGATTTGTACACAGGCCCAAGGC 600
DB 541 AGGTACATATCATTCACAGGCGCCCTGAGCTTAAAGAGATTTGTACACAGGCCCAAGGC 600
QY 601 GTGGTAGCGTTTGTGCTGATGAGCATAGCCATTGTGATGCGCGTGTCTCTCTG 660
DB 601 GTGGTAGCGTTTGTGCTGATGAGCATAGCCATTGTGATGCGCGTGTCTCTCTG 660
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DB 601 GTGGTAGCGTTTGTGCTGATGAGCATAGCCATTGTGATGCGCGTGTCTCTCTG 660
QY 661 GGCTGGAACCTCGGAGAACTGCATCTGTTTGTCTCAAGCATTTTCCACATGTGAGAA 720
DB 661 GGCTGGAACCTCGGAGAACTGCATCTGTTTGTCTCAAGCATTTTCCACATGTGAGAA 720
QY 721 ACCTACCGATGTTCTGGATCGGGGTGACACGAGCTAGCTCTTCTGTTCACTGTTATGCG 780
DB 721 ACCTACCGATGTTCTGGATCGGGGTGACACGAGCTAGCTCTTCTGTTCACTGTTATGCG 780
QY 781 TACATGATATTTCTGGAAGGCTTCAAGCCGCTCGCATGATTCAGCTGGGAC 840
DB 781 TACATGATATTTCTGGAAGGCTTCAAGCCGCTCGCATGATTCAGCTGGGAC 840
QY 841 CAGAGAGCATATCATTCACAGCTGAGATGGAAGGATGACGTTGACCCGCGCAGAC 900
DB 841 CAGAGAGCATATCATTCACAGCTGAGATGGAAGGATGACGTTGACCCGCGCAGAC 900
QY 901 CAAGCCGATGACATTTAGGTTAGCCAGAACCCCTGCTCTGATCTGTTGTTGATC 960
DB 901 CAAGCCGATGACATTTAGGTTAGCCAGAACCCCTGCTCTGATCTGTTGTTGATC 960
QY 961 ATCTGCTGGGCTCTGCTGCTTGCATATGATGATGATGATCTTTGGAGATGACAG 1020
DB 961 ATCTGCTGGGCTCTGCTGCTTGCATATGATGATGATGATCTTTGGAGATGACAG 1020
QY 1021 CTCAATTAGAGGTTTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 CTCAATTAGAGGTTTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 CCATCATCATATGCTGTGAGAGTAAAGACCTGAGACAGCTTTCCGAGATGTTTCC 1140
DB 1081 CCATCATCATATGCTGTGAGAGTAAAGACCTGAGACAGCTTTCCGAGATGTTTCC 1140
QY 1141 TCTTGTGAAGGCTGCGAGCTCTGTGATTAACAGCATGAGGAGACTGAGACTGCTGAC 1200
DB 1141 TCTTGTGAAGGCTGCGAGCTCTGTGATTAACAGCATGAGGAGACTGAGACTGCTGAC 1200
QY 1201 AAACACGAAACATGACGAGGCTTCAAGGCGCGAGAACTGATCAAGAGCAG 1260
DB 1201 AAACACGAAACATGACGAGGCTTCAAGGCGCGAGAACTGATCAAGAGCAG 1260
QY 1261 GTCAAGATTGCAAGATTAACATGCTGTGCTCAAGACAGCTGCGGAGCTCTGTA 1320
DB 1261 GTCAAGATTGCAAGATTAACATGCTGTGCTCAAGACAGCTGCGGAGCTCTGTA 1320
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RESULT 2
ADL15026
ID ADL15026 standard; DNA; 5665 BP.
XX
AC ADL15026;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human CB1 cannabinoid receptor DNA for cancer treatment.
XX
KW ds; gene; cytostatic; gene therapy; binding moiety; medicine; imaging;
KM diagnosis; prognosis; mantle cell lymphoma; cancer.
OS Homo sapiens.
PN W02003068268-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-BP001461.
XX
PR 14-FEB-2002; 2002GB-00003480.
XX
PR 29-JUN-2002; 2002GB-00015095.
XX
PA (BIOI-) BIOINVENT INT AB.
XX

PI Ek S, Borrebaeck CAK, Ehinger M;
XX WPI; 2003-697496/66.
DR P-PSDB; ADL15025.
XX
PT New compound for treating, imaging, diagnosing or prognosing mantle cell
PT lymphoma, comprises a binding moiety (e.g. antibody) that binds to a
PT protein (e.g. human autotaxin polypeptide), and a further moiety (e.g.
XX nucleic acid).
XX
PS Disclosure; SEQ ID NO 38; 342pp; English.
CC The invention relates to a compound comprising a binding moiety which
CC selectively binds to a protein or polypeptide listed in the specification
CC (e.g. human autotaxin polypeptide or human CD24 signal transducer
CC polypeptide), and a further moiety. The compound is useful in medicine or
CC in the treatment, imaging, diagnosis or prognosis of mantle cell
CC lymphomas (MCL). It is used in preparing a medicament for treating MCL, a
CC diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells
CC in the body of an individual. This sequence corresponds to a gene
CC encoding one of the polypeptides of the invention.
SQ Sequence 5665 BP; 1603 A; 1185 C; 1118 G; 1759 T; 0 U; 0 Other;
Query Match 95.4%; Score 1259.4; DB 10; Length 5665;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1263; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 52 ACTGACCTCTGGGAAAGTCCCTTCCAGAGAAAGATGATCGGGAGACAAACCCCAAGCTA 111
DB 272 ACTTCTTTAGGGGAAAGTCCCTTCCAGAGAAAGATGATCGGGAGACAAACCCCAAGCTA 331
QY 112 GTCCAGAGAGACAGAGTGAACATTAACAAATTTTACAAAGATCTCTCGTCTTCAAG 171
DB 332 GTCCAGAGAGACAGAGTGAACATTAACAAATTTTACAAAGATCTCTCGTCTTCAAG 391
QY 172 GAGATGAGAGAGACATCCAGTGTGGGAGAACTTCATGACATGAGAGTTCATGATC 231
DB 392 GAGATGAGAGAGACATCCAGTGTGGGAGAACTTCATGACATGAGAGTTCATGATC 451
QY 232 CTGAACCCAGCAGACAGTGGCCATTTGCAATCTGTCCCTCAGCGTGGGACCTTCACG 291
DB 452 CTGAACCCAGCAGACAGTGGCCATTTGCAATCTGTCCCTCAGCGTGGGACCTTCACG 511
QY 292 GTCCGTGAGAACTCTGT 351
DB 512 GTCCGTGAGAACTCTGT 571
QY 352 CTTTCTCAACATTCATGAGGAGCCTGGGCGGTGGAGACCTCTGGGGAGTGTCAATTTT 411
DB 572 CTTTCTCAACATTCATGAGGAGCCTGGGCGGTGGAGACCTCTGGGGAGTGTCAATTTT 631
QY 412 GTCTACAGCTTCAATGATCTTCCACGTGTTCACCGCAAGATAGCGCAACGTGTTCTG 471
DB 632 GTCTACAGCTTCAATGATCTTCCACGTGTTCACCGCAAGATAGCGCAACGTGTTCTG 691
QY 472 TTCAAACTGGTGGGTCAACGCGCTCTTCACTGCTCTCGTGGGACGCTGTTCTTCA 531
DB 692 TTCAAACTGGTGGGTCAACGCGCTCTTCACTGCTCTCGTGGGACGCTGTTCTTCA 751
QY 532 GCATTCGACAGGTACATATTCATTCACAGGCGCCCTGGGCGTATTAAGATGTGTCAACG 591
DB 752 GCATTCGACAGGTACATATTCATTCACAGGCGCCCTGGGCGTATTAAGATGTGTCAACG 811
QY 592 CCCAAGGCGGTGTAGCGT 651
DB 812 CCCAAGGCGGTGTAGCGT 871
QY 652 CCTCTCTGGGTGTGAATCTGGAGAAATGTCAATGTGTTGTGTGAACATTTTCCACAC 711
DB 872 CCTCTCTGGGTGTGAATCTGGAGAAATGTCAATGTGTTGTGTGAACATTTTCCACAC 931
QY 712 ATTGATGAACCTTACCTGATGTTGTGATCGGGGTCAACAGGTACTGCTTGTTCATC 771

DB 932 ATTGATGAACCTTACCTGATGTTGTGATCGGGGTCAACAGGTACTGCTTGTTCATC 991
QY 772 GTGATGCTACATGATATTTCTCTGAAAGGCTCACAGCCGCTCGCATGATTCAG 831
DB 992 GTGATGCTACATGATATTTCTCTGAAAGGCTCACAGCCGCTCGCATGATTCAG 1051
QY 832 CGTGGACCCAGAAAGACATTCATTCACAGCTGTGAGATGGAGAGTACAGGTGAC 891
DB 1052 CGTGGACCCAGAAAGACATTCATTCACAGCTGTGAGATGGAGAGTACAGGTGAC 1111
QY 892 CGGACAGACCAAGCCGACATGACATTTAGGTTAGCCAGAACCTGGTCTGTATCCGTG 951
DB 1112 CGGACAGACCAAGCCGACATGACATTTAGGTTAGCCAGAACCTGGTCTGTATCCGTG 1171
QY 952 GTGTTGATCATGTGTGGGCGCTCTGTGTAATCATGTGTATGATGTCTTTGGGAG 1011
DB 1172 GTGTTGATCATGTGTGGGCGCTCTGTGTAATCATGTGTATGATGTCTTTGGGAG 1231
QY 1012 ATGAACAAGCTCATTAAGACGTTGTTGATTTGATTTGATTTGATTTGATTTGATTTG 1071
DB 1232 ATGAACAAGCTCATTAAGACGTTGTTGATTTGATTTGATTTGATTTGATTTGATTTG 1291
QY 1072 ACCGTGAACCCCATCATGATCTGTGAGAGTAAAGACCTGCGACAGGCTTCCGAGC 1131
DB 1292 ACCGTGAACCCCATCATGATCTGTGAGAGTAAAGACCTGCGACAGGCTTCCGAGC 1351
QY 1132 ATGTTCCCTCTTGTGAAGGCACTGCGAGCCTCTGATTAACAGATGGGGAGCTCGAC 1191
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QY 1192 TGCTGTGACAAACAGGCAAAATGACAGCTGTTCACAGGCGCGCAAAAGCTGTATC 1251
DB 1412 TGCTGTGACAAACAGGCAAAATGACAGCTGTTCACAGGCGCGCAAAAGCTGTATC 1471
QY 1252 AAGACAGCGTCAAGATTGCCAAGGTAAACATGTGTGTCCAGACAGACAGCTGCGAG 1311
DB 1472 AAGACAGCGTCAAGATTGCCAAGGTAAACATGTGTGTCCAGACAGACAGCTGCGAG 1531
QY 1312 GCTGTGTGA 1320
DB 1532 GCTGTGTGA 1540
RESULT 3
AEE18784
ID AEE18784 standard; DNA; 5665 BP.
XX
AC AEE18784;
XX
DT 26-JAN-2006 (first entry)
XX
DE Human CB1 cannabinoid receptor gene (CNRL).
XX
KW Diagnosis; pharmaceutical; SNP detection; therapeutic; osteoporosis;
KW osteopathic; degeneration; endocrine disease; musculoskeletal disease;
KW cannabinoid CB1; receptor; gene; chromosome 6; ds.
XX
OS Homo sapiens.
XX
PN US2005260608-A1.
XX
PD 24-NOV-2005.
XX
PF 24-MAY-2004; 2004US-00851667.
XX
PR 24-MAY-2004; 2004US-00851667.
XX
PA (ZIMM/) ZIMMER A.
PA (KARS/) KARS M.
PA (DVER/) DE VERNEJOUL M.
PA (BAB/) BAB I.
PA (SHOH/) SHOHAMI E.

XX AC AA014003;
 XX XX 25-MAR-2003 (revised)
 DT 17-DEC-2001 (revised)
 DT 19-DEC-1991 (first entry)
 XX XX Human cannabinoid receptor coding sequence.
 DE XX Cannabis sativa; marijuana; drug test; substance K receptor; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT CDS 29..1447
 FT /tag= a
 FT /product= "human cannabinoid receptor"
 XX XX USN7564075-N.
 XX XX 03-SEP-1991.
 XX XX 08-AUG-1990; 90US-00564075.
 XX XX 08-AUG-1990; 90US-00564075.
 XX XX 08-AUG-1990; 90US-00564075.
 XX XX (USSH) NAT INST OF HEALTH.
 XX XX (USDC) US SEC OF COMMERCE.
 XX XX Matsuda L, Brownstein M;
 XX XX MPI; 1991-303326/41.
 XX XX P-PSDB; AAR14196.
 XX XX DNA encoding mammalian cannabinoid receptor - used for producing receptor
 PT for screening drugs and ligands and in detection.
 XX XX Disclousure; Fig 5; 25pp; English.
 XX XX SKKE cDNA encoding the rat cannabinoid receptor was isolated from a rat
 CC cerebral cortex cDNA library. An EcoRI-XbaI fragment was used to screen a
 CC human cosmid library. A positive clone was identified and sequenced.
 CC There is ca. 97 per cent homology between the deduced amino acid
 CC sequences of the human and rat cannabinoid receptors. (N.B. the
 CC nucleotide sequence encoding the rat cannabinoid receptor is also given
 CC in the specification but the copy quality is extremely poor; hence it is
 CC not included in N-Geneseq). Recombinantly produced receptor can be used
 CC to screen for new drugs suitable for treatment of cannabinoid-treatable
 CC conditions, e.g. glaucoma, bronchial asthma, etc. See also AAR14195.
 CC (Note: Revised NTIS applications to correct clashes with ongoing US
 CC Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-
 CC MAR-2003 to correct PA field.)
 XX XX
 SQ Sequence 1507 BP; 350 A; 428 C; 371 G; 358 T; 0 U; 0 Other;
 Query Match 95.3%; Score 1257.8; DB 2; Length 1507;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 162; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 232 CTGAACCCAGCAGAGCTGGCATTGACAGTCTGTCCTTCAAGCTGGGACCTTCACG 291
 DB 359 CTGAACCCAGCAGAGCTGGCATTGACAGTCTGTCCTTCAAGCTGGGACCTTCACG 418
 QY 292 GTCTGAGAAACCTCTGAGTCTGTGCTCATCTTCCATCCGCAAGCTCCGTCGACG 351
 DB 419 GTCTGAGAAACCTCTGAGTCTGTGCTCATCTTCCATCCGCAAGCTCCGTCGACG 478
 QY 352 CCTTCCATCAACCTTCAATCCGAGGCTGGCGGTGGCAACCTCTGGGAGAGTCAATTTT 411
 DB 479 CCTTCCATCAACCTTCAATCCGAGGCTGGCGGTGGCAACCTCTGGGAGAGTCAATTTT 538
 QY 412 GTCTACAGCTTCATTGACCTTCCAGTGTTCACAGCCGCAAGATAGCCGCAAGTGTTCG 471
 DB 539 GTCTACAGCTTCATTGACCTTCCAGTGTTCACAGCCGCAAGATAGCCGCAAGTGTTCG 598
 QY 472 TTCAAACTGGGTGGGTGACAGGCTCTTCACTGCTCTCGGTGGCAAGCTGTTCCTCA 531
 DB 599 TTCAAACTGGGTGGGTGACAGGCTCTTCACTGCTCTCGGTGGCAAGCTGTTCCTCA 658
 QY 532 GCCATCGACAGGTACATATTCATTCACAGAGCCCTGGCCTTAAGAGATTTGACACAG 591
 DB 659 GCCATCGACAGGTACATATTCATTCACAGAGCCCTGGCCTTAAGAGATTTGACACAG 718
 QY 592 CCCAAGGCGGTGTAGCGTTTGGCTGATGTGACCAATAGCCATTTGATGCGGTGTG 651
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 DB 779 CCTCTCTGGGCTGGAACTGGGAGAACTGCATCTGTTTGTCAACATTTTCCACAC 838
 QY 712 ATTGATGAACCTTACCTGATGTTCTGGATGGGGTCAACAGCTACGCTTCTGTATC 771
 DB 839 ATTGATGAACCTTACCTGATGTTCTGGATGGGGTCAACAGCTACGCTTCTGTATC 898
 QY 772 GTGTATGCGTACATGATATTTCTGTGAAGGCTCAAGCCAGCGCTTCCGATATTCAG 831
 DB 899 GTGTATGCGTACATGATATTTCTGTGAAGGCTCAAGCCAGCGCTTCCGATATTCAG 958
 QY 832 CGTGACCCGAAAGAGCATATATCCACAGCTGTGAGATGGAGAGTACAGGTAC 891
 DB 959 CGTGACCCGAAAGAGCATATATCCACAGCTGTGAGATGGAGAGTACAGGTAC 1018
 QY 892 CGGCCAAGCAAGCCCGATGAGACATTAGGTTAACCAAGCCCTGCTGATCTGTG 951
 DB 1019 CGGCCAAGCAAGCCCGATGAGACATTAGGTTAACCAAGCCCTGCTGATCTGTG 1078
 QY 952 GTGTGATCATCTGCTGGGCGCTCTGCTTGCATATGATGTGTATGATCTTTGGAG 1011
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 QY 1012 ATGAACAAAGCTATTAAGACGCTGTGATTCATCTGACATATGCTGTGCTGAACTCC 1071
 DB 1139 ATGAACAAAGCTATTAAGACGCTGTGATTCATCTGACATATGCTGTGCTGAACTCC 1198
 QY 1072 ACCGTGAACCCGATCATATATGCTGTGAGAGTAAAGACCTGGACACGCTTCCGAGC 1131
 DB 1199 ACCGTGAACCCGATCATATATGCTGTGAGAGTAAAGACCTGGACACGCTTCCGAGC 1258
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 DB 1259 ATGTTTCCCTTGTGAAGGACATGCGAGCCTCTGTGATTAACAGATGGGGAAGCTCGAC 1318
 QY 1192 TGCTTGCAAAACAGCAAAATATGACAGCTGTGTCACAGGCGCGCAAAAGCTGCATC 1251
 DB 1319 TGCTTGCAAAACAGCAAAATATGACAGCTGTGTCACAGGCGCGCAAAAGCTGCATC 1378
 QY 1252 AAGAGCAAGTCAAGTTCGAAGGTAACTATGCTGTGTCACAGACAGCTGTGCGAG 1311
 DB 1379 AAGAGCAAGTCAAGTTCGAAGGTAACTATGCTGTGTCACAGACAGCTGTGCGAG 1438
 QY 1312 GCTCTGTGA 1320

Db 1439 GCTCTGTGA 1447

|||||

RESULT 6
AB242646
ID AB242646 standard; DNA; 1755 BP.
XX
XX AB242646;
AC

XX 04-MAR-2003 (first entry)
DT

DE Human cannabinoid receptor 1 nucleotide SEQ ID NO:83.
XX

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related disease; cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer; gene; de

XX Homo sapiens.
OS

XX WO200261087-A2.
PN

XX 08-AUG-2002.
PD

XX 19-DEC-2001; 2001WO-US050107.
PP

XX 19-DEC-2000; 2000US-0257144P.
PR

XX (LIFE) LIFESPAN BIOSCIENCES INC.
PA

XX Burner GC, Roush CL, Brown JP;
PI

XX WPI; 2003-046718/04.
DR

XX P-PSDB; ABP81800.
DR

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
PT

XX Disclosure: Fig 1; 523pp; English.
PS

XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode

CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX

XX Sequence 1755 BP; 395 A; 487 C; 441 G; 432 T; 0 U; 0 Other;

Query Match 95.3%; Score 1257.8; DB 8; Length 1755;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 52 ACTGACCTCTGGGAAATGCTCTTCCAGAGAAAGATGATCTGGGAGACACCCCGACTA 111
DB 239 ACTTCTTTAGGGGAAATGCTCTTCCAGAGAAAGATGATCTGGGAGACACCCCGACTA 358
QY 112 GTCCGACGACACAGCTGAACTTACAGATTTTACACAACTCTCTGCTCTTCAAG 171
DB 359 GTCCGACGACACAGCTGAACTTACAGATTTTACACAACTCTCTCTGCTCTTCAAG 418
QY 172 GAGATGAGAGAGAAATCATCAAGTGGGGGAACTTCATGAGACATGAGTGTTCATGTC 231
DB 419 GAGATGAGAGAGAAATCATCAAGTGGGGGAACTTCATGAGACATGAGTGTTCATGTC 478
QY 232 CTGAACCCGACGACAGCTGGCCATTGCAAGTCTGTCCTTCAAGCTGGGACCTTCAAG 291
DB 479 CTGAACCCGACGACAGCTGGCCATTGCAAGTCTGTCCTTCAAGCTGGGACCTTCAAG 538
QY 292 GTCTGAGAGAACTCTGCTGCTGCTGCTCATCTCTTCAAGCTCCGACCTCGCTGACAG 351
DB 539 GTCTGAGAGAACTCTGCTGCTGCTGCTCATCTCTTCAAGCTCCGACCTCGCTGACAG 598
QY 352 CCTTCTTCACTTATGAGGAGAGCTGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
DB 599 CCTTCTTCACTTATGAGGAGAGAGCTGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 658
QY 412 GTCTACAGCTTATGATCTTCAAGCTGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 471
DB 659 GTCTACAGCTTATGATCTTCAAGCTGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 718
QY 472 TTCAAACTGGGGGTGAGCGGCTCTTCAAGCTGTTTCAAGAGAGAGAGAGAGAGAGAGAG 531
DB 719 TTCAAACTGGGGGTGAGCGGCTCTTCAAGCTGTTTCAAGAGAGAGAGAGAGAGAGAGAG 778
QY 532 GCATGACAGGATCATATTCATTCATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 591
DB 779 GCATGACAGGATCATATTCATTCATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 838
QY 592 CCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 651
DB 839 CCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 898
QY 652 CCTCTCTGGGCTGGAACCTGCGAGAACTGCATCTGTTTCTGACATTTTCCACAGC 711
DB 899 CCTCTCTGGGCTGGAACCTGCGAGAACTGCATCTGTTTCTGACATTTTCCACAGC 958
QY 712 ATTGATGAACTTACCTGATGTTTCTGATGCGGGGACACAGCTGCTCTTCTGTTATC 771
DB 959 ATTGATGAACTTACCTGATGTTTCTGATGCGGGGACACAGCTGCTCTTCTGTTATC 1018
QY 772 GTGTATGGGTACATGATATTTCTGGAAGGCTCACAGCGCGTCCGATGATTCAG 831
DB 1019 GTGTATGGGTACATGATATTTCTGGAAGGCTCACAGCGCGTCCGATGATTCAG 1078
QY 832 GTGGACCCGAGAGAGATCATTCACAGCTGTGAGATGGAGATGAGATGAGATGAGATGAG 891
DB 1079 GTGGACCCGAGAGAGATCATTCACAGCTGTGAGATGGAGATGAGATGAGATGAGATGAG 1138
QY 892 GTGGACCCGAGAGAGATCATTCACAGCTGTGAGATGGAGATGAGATGAGATGAGATGAG 951
DB 1139 GTGGACCCGAGAGAGATCATTCACAGCTGTGAGATGGAGATGAGATGAGATGAGATGAG 1198
QY 952 GTGTATGATCATGTGCTGGGGGCTCTGCTTCAATCATGATGATGATGATGATGATGATGATG 1011
DB 1199 GTGTATGATCATGTGCTGGGGGCTCTGCTTCAATCATGATGATGATGATGATGATGATGATG 1258

QY 1012 ATGAACAGCTCATTAAGACGGTGTGTCATTTGTCAGATATGCTGACCTGTGAACCTCC 1071
DB 1259 ATGAACAGCTCATTAAGACGGTGTGTCATTTGTCAGATATGCTGACCTGTGAACCTCC 1318
QY 1072 ACCGTGAACCCCATCATCATGCTCTGAGAGTAAGACCTGCGACACGCTTTCCGAGAC 1131
DB 1319 ACCGTGAACCCCATCATCATGCTCTGAGAGTAAGACCTGCGACACGCTTTCCGAGAC 1378
QY 1132 ATGTTTCCCTCTTGTGAAGGACATGCGACGCTCTGATTAACAGATGGGGGACCTCGAC 1191
DB 1379 ATGTTTCCCTCTTGTGAAGGACATGCGACGCTCTGATTAACAGATGGGGGACCTCGAC 1438
QY 1192 TGCCTGCAAAACAGCAACATGACGACGCTGTTTCAAGGGCCGCAAAAAGCTGCATC 1251
DB 1439 TGCCTGCAAAACAGCAACATGACGACGCTGTTTCAAGGGCCGCAAAAAGCTGCATC 1498
QY 1252 AAGACGACGCTCAAGATTCGCAAGGTAAACATGCTGTGTCCACAGACACGCTGCGCAG 1311
DB 1499 AAGACGACGCTCAAGATTCGCAAGGTAAACATGCTGTGTCCACAGACACGCTGCGCAG 1558
QY 1312 GCTCTGTGA 1320
DB 1559 GCTCTGTGA 1567

RESULT 7

ADN38917
ID ADN38917 standard; cDNA, 1755 BP.

XX ADN38917;

DT 17-JUN-2004 (first entry)

XX Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:235.

XX Human; differential expression; cancer; angiogenic disorder;

XX fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

XX inflammatory disease; autoimmune disease;

XX retinal neovascularisation syndrome; scarring; uterine fibroid;

XX detection; diagnosis; prognosis; drug screening; drug targeting;

XX wound healing; contraception; cytostatic; cardiac; immunomodulatory;

XX vulnery; gene therapy; vaccine; gene; ss.

XX Homo sapiens.

XX OS

XX WO2003042661-A2.

XX 22-MAY-2003.

XX 13-NOV-2002; 2002MO-US036810.

XX 13-NOV-2001; 2001US-0350666P.

XX 21-NOV-2001; 2001US-0332464P.

XX 29-NOV-2001; 2001US-0334393P.

XX 03-DEC-2001; 2001US-0335394P.

XX 14-DEC-2001; 2001US-0340376P.

XX 08-JAN-2002; 2002US-0347211P.

XX 10-JAN-2002; 2002US-0347349P.

XX 08-FEB-2002; 2002US-0355250P.

XX 13-FEB-2002; 2002US-0356714P.

XX 20-FEB-2002; 2002US-0359077P.

XX 29-MAR-2002; 2002US-036809P.

XX 04-APR-2002; 2002US-0370110P.

XX 12-APR-2002; 2002US-0372246P.

XX 05-JUN-2002; 2002US-038614P.

XX 16-JUL-2002; 2002US-0396839P.

XX 22-JUL-2002; 2002US-0397775P.

XX 22-JUL-2002; 2002US-0397845P.

XX 09-SEP-2002; 2002US-0409450P.

XX (BOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;
XX WPI; 2003-468649/44.
DR P-PSDB; ADN38918.
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
a nucleic acid in a biological sample.
PS Claim 8; SEQ ID NO 235; 1385bp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38663-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
XX

Sequence 1755 BP; 395 A; 487 C; 441 G; 432 T; 0 U; 0 Other;

Query Match 95.3%; Score 1257.8; DB 11; Length 1755;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 52 ACTGACCTCTGAGAGAGTCCCTTCCAGAGATGACTGCGGAGACACCCCACTA 111
DB 299 ACTTCTTTAAGGAGAGTCCCTTCCAGAGATGACTGCGGAGACACCCCACTA 358
QY 112 GTCCAGAGACCGAGGTAAATTTTAAACAAGTCTCTCTCTTCAAG 171
DB 359 GTCCAGAGACCGAGGTAAATTTTAAACAAGTCTCTCTCTTCAAG 418
QY 172 GAGATGAGAGAACATCAATGAGGAGAACTTCAATGACATAGATGTTTCAAGTGC 231
DB 419 GAGATGAGAGAACATCAATGAGGAGAACTTCAATGACATAGATGTTTCAAGTGC 478
QY 232 CTGAACCCAGCCAGACAGCTGCGCATTCCTGCTTCACTGCGGACCTTCAAG 291
DB 479 CTGAACCCAGCCAGACAGCTGCGCATTCCTGCTTCACTGCGGACCTTCAAG 538
QY 292 GTCTGAGAGAACTTCTGCTGCTGCTCATCTCTTCACTGCGGACCTTCAAG 351
DB 539 GTCTGAGAGAACTTCTGCTGCTGCTCATCTCTTCACTGCGGACCTTCAAG 598
QY 352 CTTTCTTCACTTCACTGAGCGAGCTGCGGAGAACTTCACTGCGGACCTTCAAG 411
DB 599 CTTTCTTCACTTCACTGAGCGAGCTGCGGAGAACTTCACTGCGGACCTTCAAG 658
QY 412 GTTACAGCTTCACTTCACTGAGCGAGCTGCGGAGAACTTCACTGCGGACCTTCAAG 471
DB 659 GTTACAGCTTCACTTCACTGAGCGAGCTGCGGAGAACTTCACTGCGGACCTTCAAG 718
QY 472 TTCAACAGTGGGTGAGCGGCTCTTCACTGCTGCGGAGAACTTCACTGCGGACCTTCAAG 531
DB 719 TTCAACAGTGGGTGAGCGGCTCTTCACTGCTGCGGAGAACTTCACTGCGGACCTTCAAG 778
QY 532 GGCATGACAGGTACATATTCATTTCAAGAGCCCTGCGCTTAAAGAGATTGTCCACAG 591
DB 779 GGCATGACAGGTACATATTCATTTCAAGAGCCCTGCGCTTAAAGAGATTGTCCACAG 838
QY 592 CCAAGGCGGTGAGCGTCTTTCCTGATGAGCAATAGCAATTTGATGCGGTGCTG 651

Db 839 CCCAAGCCGTGGTGGCTTTTTCCTGATGTGGACCATATGTCATCGCCGTGTG 898
Qy 652 CCTCTCTGGGGCTGGAACCTGGAGAACTGGCAATCTGTTTGTCTCAACAATTTTCCACAC 711
Db 899 CCTCTCTGGGGCTGGAACCTGGAGAACTGGCAATCTGTTTGTCTCAACAATTTTCCACAC 958
Qy 712 ATTGATGAAACCTACCTGATGTGTCTGGATCGGGGTCAACGAGCTACTGCTTCTGTTTCAAC 771
Db 959 ATTGATGAAACCTACCTGATGTGTCTGGATCGGGGTCAACGAGCTACTGCTTCTGTTTCAAC 1018
Qy 772 GTGATGCGTACATGATATTTCTCTGGAAAGCTCACAGCCGCTGCGATGATTTCAG 831
Db 1019 GTGATGCGTACATGATATTTCTCTGGAAAGCTCACAGCCGCTGCGATGATTTCAG 1078
Qy 832 CGTGACACCCAGAGAGCATCATCCACAGCTCTGAGAGATGGAGATACAGGTGAC 891
Db 1079 CGTGACACCCAGAGAGCATCATCCACAGCTCTGAGAGATGGAGATACAGGTGAC 1138
Qy 892 CGGCGACACCAAGCCGCGATGACATTAAGTTAGCCAAAGCCCTGGTCTGATCCGTGTG 951
Db 1139 CGGCGACACCAAGCCGCGATGACATTAAGTTAGCCAAAGCCCTGGTCTGATCCGTGTG 1198
Qy 952 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCATCATGATGTATGATGTCTTTGGAGAG 1011
Db 1199 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCATCATGATGTATGATGTCTTTGGAGAG 1258
Qy 1012 ATGAACAAGCTCATTAAGACGGTGTGTTGATCTCTGCAATGCTCTGCTGTAATCTCC 1071
Db 1259 ATGAACAAGCTCATTAAGACGGTGTGTTGATCTCTGCAATGCTCTGCTGTAATCTCC 1318
Qy 1072 ACCGTGAACCCCATCATCTATGCTCTGAGAGATGAAGACCTGCGACAGCTTCCGGAGC 1131
Db 1319 ACCGTGAACCCCATCATCTATGCTCTGAGAGATGAAGACCTGCGACAGCTTCCGGAGC 1378
Qy 1132 ATGTTTCCCTCTTGTGAAGGACCTGCGACGCTCTGATTAACAGATGAGGAGCTCGAGC 1191
Db 1379 ATGTTTCCCTCTTGTGAAGGACCTGCGACGCTCTGATTAACAGATGAGGAGCTCGAGC 1438
Qy 1192 TGCCGTGCAAAACAGCAACATGCAAGCTGATGTTTCAAGGGCCGCGAAGAGCTGCAATC 1251
Db 1439 TGCCGTGCAAAACAGCAACATGCAAGCTGATGTTTCAAGGGCCGCGAAGAGCTGCAATC 1498
Qy 1252 AAGAGCAGCTCAAGATTGCGCAAGGTAAACATGTGATGTCACAGACAGCTGCGAG 1311
Db 1499 AAGAGCAGCTCAAGATTGCGCAAGGTAAACATGTGATGTCACAGACAGCTGCGAG 1558
Qy 1312 GCTCTGTGA 1320
Db 1559 GCTCTGTGA 1567

RESULT 8
ACN38515
ID ACN38515 standard; cDNA; 5471 BP.
XX ACN38515;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) cDNA DNA324834, SEQ ID NO:2079.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KM tumour; diagnosis; cell proliferative disorder; breast cancer;
KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KM central nervous system cancer; bladder cancer; pancreatic cancer;
KM cervical cancer; melanoma; leukaemia; hybridisation probe;
KM chromosome identification; chromosome mapping; gene mapping;
KM gene therapy; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
XX MO2004030615-A2.
XX

PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
XX
PT New tumour-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 1; SEQ ID NO 2079; 7273bp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acid and polypeptide
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antigens, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention
XX
SQ Sequence 5471 BP; 1551 A; 1148 C; 1089 G; 1683 T; 0 U; 0 Other;
Query Match 95.3%; Score 1257.8; DB 13; Length 5471;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 162; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 52 ACTGACCTCTGGGAGTCCCTTCCAGAGAGATGATCTGGGGAGACACCCCAAGCTA 111
Db 214 ACTTCCTTTAGGGAGAGTCCCTTCCAGAGAGATGATCTGGGGAGACACCCCAAGCTA 273
Qy 112 GTCCAGAGACCAAGGTGAACATTACAGATTTTACAAAGTCTCTGCTCTTCAAG 171
Db 274 GTCCAGAGACCAAGGTGAACATTACAGATTTTACAAAGTCTCTGCTCTTCAAG 333
Qy 172 GAGATGAGGAGAACATTCATGTGGGAGAACTTCATGACATTAAGTGTTCATGCTC 231
Db 334 GAGATGAGGAGAACATTCATGTGGGAGAACTTCATGACATTAAGTGTTCATGCTC 393
Qy 232 CTGAACCCAGCAGAGCTGGCATTGCACTGCTGTCCTTCCAGCTGGGAGACCTTCAAG 291
Db 394 CTGAACCCAGCAGAGCTGGCATTGCACTGCTGTCCTTCCAGCTGGGAGACCTTCAAG 453
Qy 292 GTCTGAGAGAACTCTGAGTCTGTGCTCATCTTCCACTGCGAGCTTCGACAG 351
Db 454 GTCTGAGAGAACTCTGAGTCTGTGCTCATCTTCCACTGCGAGCTTCGACAG 513
Qy 352 CTTCTCAACACTTCATCTGAGCTGCGGTGGCAACCTCTGAGGAGAGTCAATTTT 411
Db 514 CTTCTCAACACTTCATCTGAGCTGCGGTGGCAACCTCTGAGGAGAGTCAATTTT 573
Qy 412 GTCTAAGCTTCATTCATTCAGTGTTCACACCGCAAGATAGCCCAAGTGTTCG 471
Db 574 GTCTAAGCTTCATTCATTCAGTGTTCACACCGCAAGATAGCCCAAGTGTTCG 633

QY 472 TTCAAACTGGGTGGGTGACGGCCCTCTTCACTGCTCCGTTGGGACGCTGTCTTCA 531
 Db 634 TTCAAACTGGGTGGGTGACGGCCCTCTTCACTGCTCCGTTGGGACGCTGTCTTCA 693
 QY 532 GCCATCGACAGTACATATTCATTCAAGGCCCCCTGAGCTTAAAGAGATTGTCAACAG 591
 Db 694 GCCATCGACAGTACATATTCATTCAAGGCCCCCTGAGCTTAAAGAGATTGTCAACAG 753
 QY 592 CCCAAGCCGTGTGAGCTTTTGGCTGATGTGACCATATGACCATTTGATGTGACGCTG 651
 Db 754 CCCAAGCCGTGTGAGCTTTTGGCTGATGTGACCATATGACCATTTGATGTGACGCTG 813
 QY 652 CCTCTCCGTGGGTGAACTGGAAGAACTGCAATCTGTTGTGAGACATTTTCCACAC 711
 Db 814 CCTCTCCGTGGGTGAACTGGAAGAACTGCAATCTGTTGTGAGACATTTTCCACAC 873
 QY 712 ATTGATGAACCTTACCTGATGTTCTGATTCGGGGTCAACAGGCTACTGCTTCTGTCATC 771
 Db 874 ATTGATGAACCTTACCTGATGTTCTGATTCGGGGTCAACAGGCTACTGCTTCTGTCATC 933
 QY 772 GTGATGCGTACATGATATTTCTGGAAGGCTCACAGCCAGCCGTCGCAATGATTCAG 831
 Db 934 GTGATGCGTACATGATATTTCTGGAAGGCTCACAGCCAGCCGTCGCAATGATTCAG 993
 QY 832 CGTGCAACCCCAAGAAAGCATCATCCACAGTCTGAGAGATGGAAAGTACAGTAC 891
 Db 994 CGTGCAACCCCAAGAAAGCATCATCCACAGTCTGAGAGATGGAAAGTACAGTAC 1053
 QY 892 CGGCGACAGCAAGCCCGCATGAGCATTTAGTTAGCAAGACCTGCTGCTGATCCTGAGT 951
 Db 1054 CGGCGACAGCAAGCCCGCATGAGCATTTAGTTAGCAAGACCTGCTGCTGATCCTGAGT 1113
 QY 952 GTGTTGATCATCTGCTGGGCCCCCTCTGCTTGCATCATGTGTATGATGTTTGGAG 1011
 Db 1114 GTGTTGATCATCTGCTGGGCCCCCTCTGCTTGCATCATGTGTATGATGTTTGGAG 1173
 QY 1012 ATGAACAGCTCATTAAGACGCTGTTTGCATTCGCAAGATGCTGCTGTCGTAACCTC 1071
 Db 1174 ATGAACAGCTCATTAAGACGCTGTTTGCATTCGCAAGATGCTGCTGTCGTAACCTC 1233
 QY 1072 ACCGGAACCCCATCATATGCTCTGAGAGATGAAGACCTGCGACAGCTTCCGAGC 1131
 Db 1234 ACCGGAACCCCATCATATGCTCTGAGAGATGAAGACCTGCGACAGCTTCCGAGC 1293
 QY 1132 ATGTTTCCCTCTTGAAGAGCATGCGACGCTCTGATTAACAGATGGGGACTCGAC 1191
 Db 1294 ATGTTTCCCTCTTGAAGAGCATGCGACGCTCTGATTAACAGATGGGGACTCGAC 1353
 QY 1192 TGCCGCAACAAACAGCAAAATGACAGCATGTTTCAAGGCGCGCAAAAGCTGACATC 1251
 Db 1354 TGCCGCAACAAACAGCAAAATGACAGCATGTTTCAAGGCGCGCAAAAGCTGACATC 1413
 QY 1252 AAGAGCAGGTCAAGATTGCAAGGTAAACATGTCTGTGTCCAGACAGACGCTGCGAG 1311
 Db 1414 AAGAGCAGGTCAAGATTGCAAGGTAAACATGTCTGTGTCCAGACAGACGCTGCGAG 1473
 QY 1312 GCTCTGTGA 1320
 Db 1474 GCTCTGTGA 1482

RESULT 9
 AEA81160
 ID AEA81160 standard; DNA; 5480 BP.

AC AEA81160;

DT 25-AUG-2005 (first entry)

DE Human cannabinoid receptor 1 (brain) variant 1 DNA.

XX screening; obesity; nutritional disorder; anorectic; ds; gene;

KW cannabinoid receptor 1.
 OS Homo sapiens.
 XX US2005136465-A1.
 PN 23-JUN-2005.
 PD 22-DEC-2004; 2004US-00019829.
 PF 22-DEC-2003; 2003EP-00104902.
 PR (CLER/) CLERC R G.
 PA (DUCH/) DUCHATEAU-NGUYEN G.
 PA (GARD/) GARDES C.
 PA (MIZR/) MIZRAHI J.
 PA (OSTE/) OSTENSON C.
 XX Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;
 PI WPI; 2005-457507/46.
 DR P-PSDB; AEA81221.
 XX Screening test compounds that reduce and/or prevent obesity involves
 PT contacting cell expressing gene from alpha-two-glycoprotein.
 PS Claim 8; SEQ ID NO 27; 21pp; English.
 CC The invention relates to a novel method for screening for test compounds
 CC that reduce and/or prevent obesity. The method comprises contacting a
 CC cell expressing a gene selected from SEQ ID NO. 1-12 or 25-85, with a
 CC compound. The method of the invention demonstrates anorectic applications
 CC and may be useful for screening for compounds that reduce and/or prevent
 CC obesity. The current sequence is that of the human cannabinoid receptor 1
 CC (brain) variant 1 DNA of the invention. The sequence listing for the
 CC specification can be located via the USPTO web-site.
 XX
 SQ Sequence 5480 BP; 1560 A; 1148 C; 1089 G; 1683 T; 0 U; 0 Other;
 Query Match 95.3%; Score 1257.8; DB 14; Length 5480;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 52 ACTGACCTCCGAGGAGTCCCTTCCAGAGAAAGTGACTGCGGGAGCAACCCCACTA 111
 Db 214 ACTGACCTCCGAGGAGTCCCTTCCAGAGAAAGTGACTGCGGGAGCAACCCCACTA 273
 QY 112 GTCCAGACAGACAGGTGAACATTACAGATTATTAACAAGTCTCTGCTTCAAG 171
 Db 274 GTCCAGACAGACAGGTGAACATTACAGATTATTAACAAGTCTCTGCTTCAAG 333
 QY 172 GAGAAATGAGGAACATTCAGTGTGGGAGAACTTCATGACATAGAGTGTTCATGTC 231
 Db 334 GAGAAATGAGGAACATTCAGTGTGGGAGAACTTCATGACATAGAGTGTTCATGTC 393
 QY 232 CTGAACCCCAACGAGCTGGCCATTGCACTGCTGCTCCATGCTGGGCACTTCAAG 291
 Db 394 CTGAACCCCAACGAGCTGGCCATTGCACTGCTGCTCCATGCTGGGCACTTCAAG 453
 QY 292 GTCTGAGAACTCTGTGTGCTGTGCTGCTCACTCCGCAAGCTTCCGCTGACAG 351
 Db 454 GTCTGAGAACTCTGTGTGCTGTGCTGCTCACTCCGCAAGCTTCCGCTGACAG 513
 QY 352 CTTTCTTACCACTTCACTTGGAGCTTGGCGGTGGGAGACCTTCTGGGGAGTCAATTTT 411
 Db 514 CTTTCTTACCACTTCACTTGGAGCTTGGCGGTGGGAGACCTTCTGGGGAGTCAATTTT 573
 QY 412 GTCTACGCTTCACTTCACTTGGAGCTTGGCGGTGGGAGACCTTCTGGGGAGTCAATTTT 471
 Db 574 GTCTACGCTTCACTTCACTTGGAGCTTGGCGGTGGGAGACCTTCTGGGGAGTCAATTTT 633
 QY 472 TTCAAACTGGGTGGGTGACGGCCCTCTTCACTGCTCCGTTGGGACGCTGTCTTCA 531

Db 634 TTCAAAGTGGGTGAGGCTGACGGCTCTTCACTGCTCCGTGGGAGCGCTGTTCTTCAACA 693
 Qy 532 GGCATCGAAGGTATCATTCATTCACAGCCCTTGGCTTATTAAGGATTTGTCAACAG 591
 Db 694 GGCATCGAAGGTATCATTCATTCACAGCCCTTGGCTTATTAAGGATTTGTCAACAG 753
 Qy 532 CCCAAGGCGGTGAGCGTTTGGCTGATGTGGAACCATAGGCAATTTGATGCGCGTGTG 651
 Db 754 CCCAAGGCGGTGAGCGTTTGGCTGATGTGGAACCATAGGCAATTTGATGCGCGTGTG 813
 Qy 652 CCTCTCTGGGCTGAACTGCGAAGAACTGCAATCTGTTTGTCTAGACATTTTCCACAC 711
 Db 814 CCTCTCTGGGCTGAACTGCGAAGAACTGCAATCTGTTTGTCTAGACATTTTCCACAC 873
 Qy 712 ATTGATGAACCTTACTGATGTTTCTGAGATCGGGGTTCACAGGATCTGCTTCTTCTATC 771
 Db 874 ATTGATGAACCTTACTGATGTTTCTGAGATCGGGGTTCACAGGATCTGCTTCTTCTATC 933
 Qy 772 GTGTATGCGTATGATATATTTCTTGGAAAGGCTCACAGCAGCGCTCCGAGATTTGAG 831
 Db 934 GTGTATGCGTATGATATATTTCTTGGAAAGGCTCACAGCAGCGCTCCGAGATTTGAG 993
 Qy 832 CCGTGCACCCAGAGAGCATCATTCACACGCTGAGAGATGGAAAGGTACAGGTGACC 891
 Db 994 CCGTGCACCCAGAGAGCATCATTCACACGCTGAGAGATGGAAAGGTACAGGTGACC 1053
 Qy 892 CGGCGAAGCCAGAGCGCGCATGACATTTAGGTTAGCCAGAGCCCTGCTTCTGATCTGCTG 951
 Db 1054 CGGCGAAGCCAGAGCGCGCATGACATTTAGGTTAGCCAGAGCCCTGCTTCTGATCTGCTG 1113
 Qy 952 GTGTATGATCATGTGCTGGGCGCCCTGCTGCTTGAATCATGATGATGATGATGATGATG 1011
 Db 1114 GTGTATGATCATGTGCTGGGCGCCCTGCTGCTTGAATCATGATGATGATGATGATGATG 1173
 Qy 1012 ATGAACAGGCTCATTAAAGCGGTGTTTGAATTTCTGCAAGTATCTGCTGCTGTAATCC 1071
 Db 1174 ATGAACAGGCTCATTAAAGCGGTGTTTGAATTTCTGCAAGTATCTGCTGCTGTAATCC 1233
 Qy 1072 ACCGGAACCCCATATCATTTAGCTTGAAGATTAAGACCTGCGACAGCTTTCCGAGAC 1131
 Db 1234 ACCGGAACCCCATATCATTTAGCTTGAAGATTAAGACCTGCGACAGCTTTCCGAGAC 1293
 Qy 1132 ATGTTTCCCTCTTGAAGAGCATGCGAGCCTCTGATTAACAGATGGGGAGCTCGAGC 1191
 Db 1294 ATGTTTCCCTCTTGAAGAGCATGCGAGCCTCTGATTAACAGATGGGGAGCTCGAGC 1353
 Qy 1192 TGCTGCAACAACAGCAACATGCAAGTGTTCACAGGCGCGAGAAAGCTGCAATC 1251
 Db 1354 TGCTGCAACAACAGCAACATGCAAGTGTTCACAGGCGCGAGAAAGCTGCAATC 1413
 Qy 1252 AAGAGCAGGTCAGATTTGCCAAGGTAAACATGTCGTGTCCACAGACAGTCTGCCAG 1311
 Db 1414 AAGAGCAGGTCAGATTTGCCAAGGTAAACATGTCGTGTCCACAGACAGTCTGCCAG 1473
 Qy 1312 GCTCTGTGA 1320
 Db 1474 GCTCTGTGA 1482

RESULT 10
 ADA24536
 ID ADA24536 standard; cDNA; 5653 BP.
 AC ADA24536;
 XX
 XX 20-NOV-2003 (first entry)
 DE Human cDNA differential expressed in adipose tissue, INCTYB1383759.1.
 XX
 XX

KW ss; differential expression; adipose tissue; cytoskeletal; hypotensive;
 KW antiatherosclerotic; antidiabetic; anorectic; gene therapy;
 KW peroxisome proliferator-activated receptor gamma; PPARgamma;
 KW diabetes mellitus; obesity; hypertension; atherosclerosis; breast cancer;

KW prostate cancer; colon cancer; polycystic ovarian syndrome.
 XX Homo sapiens.
 OS
 XX
 PN US2003096272-A1.
 XX
 XX 22-MAY-2003.
 PD
 XX 29-JUL-2002; 2002US-00208408.
 PF
 XX 30-JUL-2001; 2001US-0308868P.
 PR
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX
 XX Scheyde XM;
 PI
 XX WPI; 2003-606416/57.
 DR
 XX
 PT New combination comprising several cDNAs, useful for preparing a
 PT composition for diagnosing or treating diabetes mellitus, obesity,
 PT hypertension, atherosclerosis, or cancer of the breast, prostate or
 PT colon.
 PS
 XX Claim 1; Page 75-77; 84pp; English.

CC Then invention relates to a new combination comprising 55 cDNAs (ADA24485
 CC -ADA24539) or their complements that are differentially regulated in an
 CC adipose sample. Also included are detecting differential expression of
 CC one or more cDNAs in a sample containing nucleic acids, screening several
 CC molecules or compounds to identify a ligand that specifically binds a
 CC cDNA, a vector comprising the cDNA, a host cell containing the vector,
 CC producing a protein, screening several molecules or compounds, producing
 CC an antibody and the isolated antibody. The cDNAs comprise sequences which
 CC are upregulated or downregulated in response to peroxisome proliferator-
 CC activated receptor gamma (PPARgamma) agonist. The combination comprising
 CC several cDNAs is useful for preparing a composition for diagnosing or
 CC treating diabetes mellitus, obesity, hypertension, atherosclerosis, or
 CC cancer of the breast, prostate or colon, or polycystic ovarian syndrome.
 CC
 XX Sequence 5653 BP; 1601 A; 1185 C; 1117 G; 1750 T; 0 U; 0 Other;

Query Match 95.3%; Score 1257.8; DB 9; Length 5653;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 52 ACTGACCTCTGGAAGTCCCTTCCAGAGAAATGATGCTGCGGAGACAAACCCCAAGCTA 111
 Db 260 ACTTCTTTAGGGGAAGTCCCTTCCAGAGAAATGATGCTGCGGAGACAAACCCCAAGCTA 319
 Qy 112 GTCCAGAGACAGGTGAACATTACAGATTTTAAACAAGTCTCTGCTCTTCAAG 171
 Db 320 GTCCAGAGACAGGTGAACATTACAGATTTTAAACAAGTCTCTGCTCTTCAAG 379
 Qy 172 GAGATGAGGAGATCATCATGTGGGAGAACTTCAATGACATTAAGTGTTCATGCTC 231
 Db 380 GAGATGAGGAGATCATCATGTGGGAGAACTTCAATGACATTAAGTGTTCATGCTC 439
 Qy 232 CTGAACCCAGCAGAGCTGGCCATTGCACTGCTGCTTCCACAGCTGGGACCTTCAAG 291
 Db 440 CTGAACCCAGCAGAGCTGGCCATTGCACTGCTGCTTCCACAGCTGGGACCTTCAAG 499
 Qy 292 GTCTGAGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 351
 Db 500 GTCTGAGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 559
 Qy 352 CCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 411
 Db 560 CCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 619
 Qy 412 GTTACAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 471
 Db 620 GTTACAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 679

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QY 472 TTCAAACTGGTGGGGTCAAGGCGCTCTTCACTGGCCCTCGTGGGAGCGCTGTCTCTCA 531
DB 680 TTCAAACTGGTGGGGTCAAGGCGCTCTTCACTGGCCCTCGTGGGAGCGCTGTCTCTCA 739
QY 532 GCCATCGACAGGTACATATTCATTCACAGGCCCTTGCCCTATTAAGAGATTGTCCACAG 591
DB 740 GCCATCGACAGGTACATATTCATTCACAGGCCCTTGCCCTATTAAGAGATTGTCCACAG 799
QY 592 CCCAAGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 651
DB 800 CCCAAGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 859
QY 652 CCTCTCTGGGCTGGAACTGGAGAAACTGCAATCTGTTTGCTGACATTTTCCACAC 711
DB 860 CCTCTCTGGGCTGGAACTGGAGAAACTGCAATCTGTTTGCTGACATTTTCCACAC 919
QY 712 ATTGAATGAACCTTACCTGATGTTCTGATTCGGGGTCAACAGGTACTGCTTCTGTTCATC 771
DB 920 ATTGAATGAACCTTACCTGATGTTCTGATTCGGGGTCAACAGGTACTGCTTCTGTTCATC 979
QY 772 GTGATGGGTACATGATATATCTCTGGAAGGTCAACCCAGCCGCTCCGATGATTGAG 831
DB 980 GTGATGGGTACATGATATATCTCTGGAAGGTCAACCCAGCCGCTCCGATGATTGAG 1039
QY 832 CGTGGCACCAGAAAGAGATCATCATCAACAGTCTGAGATGGGAAGTACAGGTGACC 891
DB 1040 CGTGGCACCAGAAAGAGATCATCATCAACAGTCTGAGATGGGAAGTACAGGTGACC 1099
QY 892 CGGCCAGACCAAGCCCGCATGACATTAGTTAGCCAAAGACCCTGTGCTTGAATCTGTGTG 951
DB 1100 CGGCCAGACCAAGCCCGCATGACATTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 1159
QY 952 GTGTTGATCATCTGCTGGGGCCCTGCTGCTGCAATCAGTGTATGATGCTTTGGGAG 1011
DB 1160 GTGTTGATCATCTGCTGGGGCCCTGCTGCTGCAATCAGTGTATGATGCTTTGGGAG 1219
QY 1012 ATGAACAAGCTCATTAAGACGGTGTTCATTTCTGACATAGCTCTGCTGCTGAACTCC 1071
DB 1220 ATGAACAAGCTCATTAAGACGGTGTTCATTTCTGACATAGCTCTGCTGCTGAACTCC 1279
QY 1072 ACCGTGAACCCCATCATATGCTCTGAGAGTAAGAACTTGGACAGCGCTTTCGGAGC 1131
DB 1280 ACCGTGAACCCCATCATATGCTCTGAGAGTAAGAACTTGGACAGCGCTTTCGGAGC 1339
QY 1132 ATGTTTCCCTCTTGGAGAGCACTGGAGCCTCTGGAATACAGATAGGGGACCTCGGAC 1191
DB 1340 ATGTTTCCCTCTTGGAGAGCACTGGAGCCTCTGGAATACAGATAGGGGACCTCGGAC 1399
QY 1192 TGCCCTGCAAAACAGCAAAACATGCAAGCTGTTTCAAGGGCCGCAAAAAGCTGCATC 1251
DB 1400 TGCCCTGCAAAACAGCAAAACATGCAAGCTGTTTCAAGGGCCGCAAAAAGCTGCATC 1459
QY 1252 AAGAGCAGGTCAAGATTGCGCAAGGTAAACATGCTGTGTCTCAGACACGCTTCCGAG 1311
DB 1460 AAGAGCAGGTCAAGATTGCGCAAGGTAAACATGCTGTGTCTCAGACACGCTTCCGAG 1519
QY 1312 GCTCTGTGA 1320
DB 1520 GCTCTGTGA 1528
```

RESULT 11

ID ADH77049 standard; DNA; 1419 BP.

XX ADH77049;

XX 22-APR-2004 (first entry)

XX hCB-1 double constitutive mutant encoding DNA, SEQ ID 2.

XX Anorectic; neuroprotective; cardiovascular; respiratory;
XX gastrointestinal; cannabinoid; CB₁ receptor; obesity; psychiatric;

KW neurological; immune; cardiovascular; reproductive; endocrine; disorder;
KW respiratory; gastrointestinal; hCB-1 D213A; mutant; ds.

OS Homo sapiens.

XX Synthetic.

PN WO2004008150-A1.

XX 22-JAN-2004.

XX 14-JUL-2003; 2003WO-GB003066.

XX 17-JUL-2002; 2002SR-00002242.

XX (ASTR) ASTRAZENCA AB.

PA (ASTR) ASTRAZENCA UK LTD.

XX Greasley P;

DR WPI; 2004-143121/14.

PT Identifying an inverse agonist of a cannabinoid (CB) receptor, useful in

PT treating obesity, psychiatric and neurological disorders, comprises

PT contacting a test inhibitory agent with constitutively active CB

PS Claim 24; SEQ ID NO 2; 31pp; English.

CC The invention relates to a method for identifying an inverse agonist of a

CC cannabinoid (CB) receptor comprising contacting a CB receptor test

CC inhibitory agent with the cell expressing the constitutively active CB

CC receptor. The method is useful in identifying an inverse agonist of a CB

CC receptor. The true antagonist or inverse agonist is useful in preparing a

CC medicament for treating or preventing a disorder associated with a CB

CC receptor. The disorder is obesity, psychiatric and neurological

CC disorders. They are also useful in treating immune cardiovascular,

CC reproductive and endocrine disorders and also diseases related to

CC respiratory and gastrointestinal systems. The current sequence represents

CC the hCB-1 double constitutive mutant encoding DNA.

XX Sequence 1419 BP; 320 A; 410 C; 355 G; 334 T; 0 U; 0 Other;

XX Query Match 95.2%; Score 1256.2; DB 12; Length 1419;

XX Best Local Similarity 99.4%; Pred. No. 0;

XX Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 52 ACTGACCTCTGGGAGTCCCTTCCAAAGAGATGACTGCGGAGACACCCAGCTA 111

DB 151 ACTTCTTTAGGGGAAGTCCCTTCCAAAGAGATGACTGCGGAGACACCCAGCTA 210

QY 112 GTCCAGAGACCGAGTGAACATTAAGAAATTTTACAAGTCTCTGCTCTTCAAG 171

DB 211 GTCCAGAGACCGAGTGAACATTAAGAAATTTTACAAGTCTCTGCTCTTCAAG 270

QY 172 GAGATGAGAGAAATCATCAAGTGTGGGAGAACTTCAATGACATATAGTGTTCATGTC 231

DB 271 GAGATGAGAGAAATCATCAAGTGTGGGAGAACTTCAATGACATATAGTGTTCATGTC 330

QY 232 CTGAACCCAGCAGAGCTGGCAATGCACTGTCTGCTCTGACAGCTGGGACCTTCAAG 291

DB 331 CTGAACCCAGCAGAGCTGGCAATGCACTGTCTGCTCTGACAGCTGGGACCTTCAAG 390

QY 292 GTCCCTGAGAAACCTCTGGGTGCTGAGTCAATCTTCCAGCTCCGAGCTCCGCTGAGG 351

DB 391 GTCCCTGAGAAACCTCTGGGTGCTGAGTCAATCTTCCAGCTCCGAGCTCCGCTGAGG 450

QY 352 CTTTCTACACATTCATCGAGCGCTGGCGGTGGCAAGCTCTGAGGAGTGTCAATTTT 411

DB 451 CTTTCTACACATTCATCGAGCGCTGGCGGTGGCAAGCTCTGAGGAGTGTCAATTTT 510

QY 412 GTCTACAGCTTCATTAATTCATCGTGTTCACCGCAAGATTAACCGCAAGTGTTCG 471

DB 511 GTCTACAGCTTCATTAATTCATCGTGTTCACCGCAAGATTAACCGCAAGTGTTCG 570

QY 472 TTCAAACTGGGTGGGTCACGGGCTCTTCACTGCTCCGTGGGGACCTGTTCTTCA 531
 Db 571 TTCAAACTGGGTGGGTCACGGGCTCTTCACTGCTCCGTGGGGACCTGTTCTTCA 630
 QY 532 GCCATGACAGGTATCATTCATTCAAGGCCCTGGGCTATTAAGAGATTGTCAACAG 591
 Db 631 GCCATGACAGGTATCATTCATTCAAGGCCCTGGGCTATTAAGAGATTGTCAACAG 690
 QY 592 CCCAAGGCGGTGTAGCGTTTGGCTGTGATGTGACCAATGACATTGTATGCGCGTGT 651
 Db 691 CCCAAGGCGGTGTAGCGTTTGGCTGTGATGTGACCAATGACATTGTATGCGCGTGT 750
 QY 652 CCTCTCTGGGGCTGGAATGCGGGAATCTGTTTGTCTCAACATTTTCCACAC 711
 Db 751 CCTCTCTGGGGCTGGAATGCGGGAATCTGTTTGTCTCAACATTTTCCACAC 810
 QY 712 ATTTGAATGAACCTACTGATGTTCTGATCGGGGTCAAGCAGCTACTGCTTCTGATC 771
 Db 811 ATTTGAATGAACCTACTGATGTTCTGATCGGGGTCAAGCAGCTACTGCTTCTGATC 870
 QY 772 GTGTATGCTATGATATATTTCTTGAAGGCTCAAGCCAGCGCTGCGCATGATCAG 831
 Db 871 GTGTATGCTATGATATATTTCTTGAAGGCTCAAGCCAGCGCTGCGCATGATCAG 930
 QY 832 CGTGGACCCAGAGAGCATCATCCACAGTCTGAGAGATGGAGAGTACAGGTGACC 891
 Db 931 CGTGGACCCAGAGAGCATCATCCACAGTCTGAGAGATGGAGAGTACAGGTGACC 990
 QY 892 CGGCGACAGCAAGCCGCGATGACATTAAGTATGACCAAGACCCTGCTGATCCGAGT 951
 Db 991 CGGCGACAGCAAGCCGCGATGACATTAAGTATGACCAAGACCCTGCTGATCCGAGT 1050
 QY 952 GTGTGATCATCTGCTGGGGCCCTCTGCTTGAATCATGATGATGATGATGATGATG 1011
 Db 1051 GTGTGATCATCTGCTGGGGCCCTCTGCTTGAATCATGATGATGATGATGATGATG 1110
 QY 1012 ATGAACAAGCTATTAAGAGCGTGTGATGATCTGCAAGATGCTGCTGCTGCAACTC 1071
 Db 1111 ATGAACAAGCTATTAAGAGCGTGTGATGATCTGCAAGATGCTGCTGCTGCAACTC 1170
 QY 1072 ACCGTGAACCCCATCATCTATGCTCTGAAGAGTAAAGACCTGCGACAGCTTCCGAGC 1131
 Db 1171 ACCGTGAACCCCATCATCTATGCTCTGAAGAGTAAAGACCTGCGACAGCTTCCGAGC 1230
 QY 1132 ATGTTTCCCTCTTGAAGAGCACTGCGACGCTCTGATTAACAGCATGGGGGACTCGAC 1191
 Db 1231 ATGTTTCCCTCTTGAAGAGCACTGCGACGCTCTGATTAACAGCATGGGGGACTCGAC 1290
 QY 1192 TGCCGCAACAACAGCAACAATGACAGCATGTTTCAAGGGCCGCAAAAGCTGCAATC 1251
 Db 1291 TGCCGCAACAACAGCAACAATGACAGCATGTTTCAAGGGCCGCAAAAGCTGCAATC 1350
 QY 1252 AAGACAGCGTCAAGATTGCAAGGTAAACATGTCTGTGTCAGACAGCATCTGCGAG 1311
 Db 1351 AAGACAGCGTCAAGATTGCAAGGTAAACATGTCTGTGTCAGACAGCATCTGCGAG 1410
 QY 1312 GCTCTGTGA 1320
 Db 1411 GCTCTGTGA 1419

RESULT 12

ADH77050 standard; DNA; 1419 BP.

ADH77050;

22-APR-2004 (first entry)

hCB-1-D213A constitutive mutant encoding DNA, SEQ ID 3.

Anorectic; neuroprotective; cardiovascular; respiratory;

KW Gastrointestinal; cannabinoid; CB; receptor; obesity; psychiatric;
 KW neurological; immune; cardiovascular; reproductive; endocrine; disorder;
 KW respiratory; gastrointestinal; hCB-1 D213A; mutant; ds.
 OS Homo sapiens.
 OS Synthetic.
 PN MO2004008150-A1.
 XX
 PD 22-JAN-2004.
 XX
 PF 14-JUL-2003; 2003MO-GB003066.
 XX
 PR 17-JUL-2002; 2002SE-00002242.
 XX
 PA (ASTR) ASTRAZENECA AB.
 PA (ASTR) ASTRAZENECA UK LTD.
 PI Greasley P;
 XX
 DR WPI; 2004-143121/14.
 XX
 PT Identifying an inverse agonist of a cannabinoid (CB) receptor, useful in
 PT treating obesity, psychiatric and neurological disorders, comprises
 PT contacting a test inhibitory agent with constitutively active CB
 PT receptor.
 PS
 PS Claim 24; SEQ ID NO 3; 31pp; English.
 XX
 CC The invention relates to a method for identifying an inverse agonist of a
 CC cannabinoid (CB) receptor comprising contacting a CB receptor test
 CC inhibitory agent with the cell expressing the constitutively active CB
 CC receptor. The method is useful in identifying an inverse agonist of a CB
 CC receptor. The true antagonist or inverse agonist is useful in preparing a
 CC medicament for treating or preventing a disorder associated with a CB
 CC receptor. The disorder is obesity, psychiatric and neurological
 CC disorders. They are also useful in treating immune cardiovascular,
 CC reproductive and endocrine disorders and also diseases related to
 CC respiratory and gastrointestinal systems. The current sequence represents
 CC the hCB-1-D213A constitutive mutant encoding DNA.
 XX
 SQ Sequence 1419 BP; 320 A; 410 C; 355 G; 334 T; 0 U; 0 Other;
 Query Match 95.2%; Score 1256.2; DB 12; Length 1419;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 52 ACTGACCTCTGGGAAGTCCCTTCCAGAGAAAGATGACTGGGGAGACACCCGAGCTA 111
 Db 151 ACTTCTTTAGGGGAAGTCCCTTCCAGAGAAAGATGACTGGGGAGACACCCGAGCTA 210
 QY 112 GTCCAGAGACAGAGTGAACATTACAGAAATTTTCAACAAGTCTCTGCTCTTCAAG 171
 Db 211 GTCCAGAGACAGAGTGAACATTACAGAAATTTTCAACAAGTCTCTGCTCTTCAAG 270
 QY 172 GAGAAATGAGAGAACATTCAGTGTGGGAGAACTTTCATGACATTAAGTGTTCATGTC 231
 Db 271 GAGAAATGAGAGAACATTCAGTGTGGGAGAACTTTCATGACATTAAGTGTTCATGTC 330
 QY 232 CTGAACCCGACGACAGCTGCGCAATTCAGTCTGTCCTTCAAGCTGCGGACCTTTCAG 291
 Db 331 CTGAACCCGACGACAGCTGCGCAATTCAGTCTGTCCTTCAAGCTGCGGACCTTTCAG 390
 QY 292 GTCTGAGAACTCTCTGTGTGTGCTGATTCCTCACTCCGAGCTGCGCTGCAAG 351
 Db 391 GTCTGAGAACTCTCTGTGTGTGCTGATTCCTCACTCCGAGCTGCGCTGCAAG 450
 QY 352 CTTTCTTACCACTTTCATGAGAGCTGCGGTGGAGACCTTCTGGGGAGTGTATTTT 411
 Db 451 CTTTCTTACCACTTTCATGAGAGCTGCGGTGGAGACCTTCTGGGGAGTGTATTTT 510
 QY 412 GTCTACAGCTTCATGATTCAGAGTGTTCACAGCGCAAGATAGCCGAGTGTTCG 471

Db 511 GTCTACAGCTTCATTGACTTCCACGCTGTTCCACCCGCAAGATAGCCGCAACGCTGTTCTG 570
 Qy 472 TTCAACTGGGAGGGGTCAAGCGCTCCTTCACTGCTCCGAGGAGAGCTGTTCTTCTCA 531
 Db 571 TTCAACTGGGAGGGGTCAAGCGCTCCTTCACTGCTCCGAGGAGAGCTGTTCTTCTCA 630
 Qy 532 GCCATCGACAGGTACATATCCATTGCAAGGCCCCCTGAGCTATAGAGATTTGCAACAG 591
 Db 631 GCCATCGACAGGTACATATCCATTGCAAGGCCCCCTGAGCTATAGAGATTTGCAACAG 690
 Qy 552 CCCAAGCGCGTGTAGCGCTTTGCTGATGTGACCAATAGCCATTGTGTAGCGCGCTGTG 651
 Db 691 CCCAAGCGCGTGTAGCGCTTTGCTGATGTGACCAATAGCCATTGTGTAGCGCGCTGTG 750
 Qy 652 CCTCTCTGGGGTGGAACTGGAGAAACCTGCAATCTGTTTGTCTGAGACTTTTCCACAC 711
 Db 751 CCTCTCTGGGGTGGAACTGGAGAAACCTGCAATCTGTTTGTCTGAGACTTTTCCACAC 810
 Qy 712 ATTGATGAAGCTTACCTGATGTTCTGAAATCGGGGTCAACAGCGTACTGCTTCTGTTCA 771
 Db 811 ATTGATGAAGCTTACCTGATGTTCTGAAATCGGGGTCAACAGCGTACTGCTTCTGTTCA 870
 Qy 772 GTGTATGCGTACATGATATTTCTTGAAAGGCTCAACAGCCGCTCCGATGATTCAG 831
 Db 871 GTGTATGCGTACATGATATTTCTTGAAAGGCTCAACAGCCGCTCCGATGATTCAG 930
 Qy 832 CGTGACACCCGAAGAGATCATCATCAACAGCTGAGAGATGGAGGTACAGGTAGACC 891
 Db 931 CGTGACACCCGAAGAGATCATCATCAACAGCTGAGAGATGGAGGTACAGGTAGACC 990
 Qy 892 CGGCGAGACCAAGCCCGCATGAGCAATTAGGTTAGCCAAAGACCCTGATCTCTGATCTG 951
 Db 991 CGGCGAGACCAAGCCCGCATGAGCAATTAGGTTAGCCAAAGACCCTGATCTCTGATCTG 1050
 Qy 952 GTGTGATCATGTGCTGGGGCCCTCTGCTTGGAATCATAGGTATGATGTTCTTTGGAG 1011
 Db 1051 GTGTGATCATGTGCTGGGGCCCTCTGCTTGGAATCATAGGTATGATGTTCTTTGGAG 1110
 Qy 1012 ATGAACAAGCTCATTAAGACGAGTGTGTCATCTGCAAGTATCTGCTGCTGTAACCTCC 1071
 Db 1111 ATGAACAAGCTCATTAAGACGAGTGTGTCATCTGCAAGTATCTGCTGCTGTAACCTCC 1170
 Qy 1072 ACCGTGAACCCCATCATCTATGCTCTGAGAGATGAAGACCTGCGACACGCTTTCCGAG 1131
 Db 1171 ACCGTGAACCCCATCATCTATGCTCTGAGAGATGAAGACCTGCGACACGCTTTCCGAG 1230
 Qy 1132 ATGTTTCCCTCTTGTGAAGGCACTGCGACGCTCTGATATACAGCATGGGGGACTTCGAC 1191
 Db 1231 ATGTTTCCCTCTTGTGAAGGCACTGCGACGCTCTGATATACAGCATGGGGGACTTCGAC 1290
 Qy 1192 TGCCGTGCAAAACAGCAAAACATGACGAGCTGTTTCAACAGGGCCGCAAGAAAGCTGCATC 1251
 Db 1251 TGCCGTGCAAAACAGCAAAACATGACGAGCTGTTTCAACAGGGCCGCAAGAAAGCTGCATC 1350
 Qy 1252 AAGACACGCGTCAGATTGCGCAAGGTAAACATGTCTGTGTTCCACAGACACGCTCTCCGAG 1311
 Db 1351 AAGACACGCGTCAGATTGCGCAAGGTAAACATGTCTGTGTTCCACAGACACGCTCTCCGAG 1410
 Qy 1312 GCTCTGTGA 1320
 Db 1411 GCTCTGTGA 1419

RESULT 13

ADO29849 standard; cDNA, 1419 BP.

ADO29849;

29-JUL-2004 (first entry)

Human GPCR CNR1 polynucleotide, SEQ ID NO:951.

XX

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antiemetic;
 KW cytoskeletal; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhetic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW gene; ss.
 OS Homo sapiens.
 PN WO2004040000-A2.
 PD 13-MAY-2004.
 XX 09-SEP-2003; 2003WO-US028226.
 PF 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX (PRIM-) PRIMAL INC.
 PA Galtanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,
 PI Madisen J, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX MPI; 2004-390329/36.
 DR P-PSDB; ADO29261.
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 PS Claim 151, SEQ ID NO 951; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, thymus and
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, ovary,
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
 CC nucleic acid of the invention. Note: The full sequence data for this
 CC patent did not form part of the printed specification; those sequences
 CC not shown were obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1419 BP; 322 A; 409 C; 354 G; 334 T; 0 U; 0 Other;
SQ Query Match 95.2%; Score 1256.2; DB 12; Length 1419;
Beet Local Similarity 99.4%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 52 ACTGACCTCTGGAAGTCCCTTCCAGAGATGATGCGGGAGACACCCCGACTA 111
DB 151 ACTTCTTTAGGGGAAGTCCCTTCCAGAGAGATGATGCGGGAGACACCCCGACTA 210
QY 112 GTCCAGACAGACAGAGTGAACATTACAGATTTTACAGAGTCTCTGTCCTTCAAG 171
DB 211 GTCCAGACAGACAGAGTGAACATTACAGATTTTACAGAGTCTCTGTCCTTCAAG 270
QY 172 GAGATGAGAGAGAAATCCAGTGTGGGAGAACTTATGATGACATAGAGTTTCAATGTC 231
DB 271 GAGATGAGAGAGAAATCCAGTGTGGGAGAACTTATGATGACATAGAGTTTCAATGTC 330
QY 232 CTGAACCCAGCAGCAGAGTGGCAATTGAGTCTGTCCTTCCAGCCTGAGCCTTCAAG 291
DB 331 CTGAACCCAGCAGCAGAGTGGCAATTGAGTCTGTCCTTCCAGCCTGAGCCTTCAAG 390
QY 292 GTCTGAGAGAACTCTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 351
DB 391 GTCTGAGAGAACTCTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 450
QY 352 CCTTCTTCAACATTATGATGAGAGCCTGAGGAGTGGAGACCTCTGAGGAGTGTCAATTTT 411
DB 451 CCTTCTTCAACATTATGATGAGAGCCTGAGGAGTGGAGACCTCTGAGGAGTGTCAATTTT 510
QY 412 GTCTGAGAGTTCATGATTCATGATTCATGATTCATGATTCATGATTCATGATTCATG 471
DB 511 GTCTGAGAGTTCATGATTCATGATTCATGATTCATGATTCATGATTCATGATTCATG 570
QY 472 TTCAAACTGGGTGGGTGCAAGGCTCTTCACTGTCCTGTCGAGGAGCTGTCCTTCA 531
DB 571 TTCAAACTGGGTGGGTGCAAGGCTCTTCACTGTCCTGTCGAGGAGCTGTCCTTCA 630
QY 532 GCCATGACAGATCATATCCATTCACAGGCCCCCTGAGGCTTAAAGAGATTGTCAACAG 591
DB 631 GCCATGACAGATCATATCCATTCACAGGCCCCCTGAGGCTTAAAGAGATTGTCAACAG 690
QY 592 CCCAAGGCGGTGATGCGTTTGGCTGATGTCGATGTCGATGTCGATGTCGATGTCGATG 651
DB 691 CCCAAGGCGGTGATGCGTTTGGCTGATGTCGATGTCGATGTCGATGTCGATGTCGATG 750
QY 652 CCTCTCTGGGTGAGACTGCGAGAACTGCAATCTGTTTGTCTAGACATTTTCCACAGC 711
DB 751 CCTCTCTGGGTGAGACTGCGAGAACTGCAATCTGTTTGTCTAGACATTTTCCACAGC 810
QY 712 ATTGATGAACCTTACCTGATGTTCTGATGCGGGGTACACAGCTGATGCTTGTTCATC 771
DB 811 ATTGATGAACCTTACCTGATGTTCTGATGCGGGGTACACAGCTGATGCTTGTTCATC 870
QY 772 GGTATGAGTACATGATATTTCTGGAAGGTCACAGCAGCCGTCGATGATGATGATGATG 831
DB 871 GGTATGAGTACATGATATTTCTGGAAGGTCACAGCAGCCGTCGATGATGATGATGATG 930
QY 832 CGTGGCACCAGAGAGATCATTCACACAGCTGAGAGTGGAGAGTACAGGTGAC 891
DB 931 CGTGGCACCAGAGAGATCATTCACACAGCTGAGAGTGGAGAGTACAGGTGAC 990
QY 892 CGGCGACAGCAAGCCCGCATGAGCAATTAGGTCAGCAAGCCTGTGCTGATCTTGTG 951
DB 991 CGGCGACAGCAAGCCCGCATGAGCAATTAGGTCAGCAAGCCTGTGCTGATCTTGTG 1050
QY 952 GTGTTGATCATCTGTGGGGCCCTGCTGTCGATCATGAGTGTATGATGATGATGATG 1011
DB 1051 GTGTTGATCATCTGTGGGGCCCTGCTGTCGATCATGAGTGTATGATGATGATGATG 1110
QY 1012 ATGAACAAAGCTCATTAAGACGGTGTTCGATTCAGATGCTGCTGCTGTAACCTCC 1071

DB 1111 ATGAACAAAGCTCATTAAGACGGTGTTCGATTCAGATGCTGCTGCTGTAACCTCC 1170
QY 1072 ACCGTGAACCCCATCATATGCTCTGAGAGATGAGACCTGACAGCTTTCGGAGC 1131
DB 1171 ACCGTGAACCCCATCATATGCTCTGAGAGATGAGACCTGACAGCTTTCGGAGC 1230
QY 1132 ATGTTTCCCTCTTGTGAAGGCACTGCGAGCCTTGGATTAACAGCATGGGGAGCTCGAC 1191
DB 1231 ATGTTTCCCTCTTGTGAAGGCACTGCGAGCCTTGGATTAACAGCATGGGGAGCTCGAC 1290
QY 1192 TGCCTGCAAAACAGCAAAACATGACAGCAAGTTCACAGGCGCCAGAAAAGCTGCATC 1251
DB 1291 TGCCTGCAAAACAGCAAAACATGACAGCAAGTTCACAGGCGCCAGAAAAGCTGCATC 1350
QY 1253 AAGAGCAGGTCAAGATTGCGCAAGTAACTATGTCGTGTCACAGACAGCTTCGGAG 1311
DB 1351 AAGAGCAGGTCAAGATTGCGCAAGTAACTATGTCGTGTCACAGACAGCTTCGGAG 1410
QY 1312 GCTGTGTA 1320
DB 1411 GCTGTGTA 1419

RESULT 14
ABZ35604
ID ABZ35604 strand; cDNA; 2135 BP.
XX AC ABZ35604;
XX DT 05-FEB-2003 (first entry)
XX DE Human gene expression profile polynucleotide seq ID NO 715.
XX KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
XX KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
XX KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
XX KW gene expression; gene; ss.
XX OS Homo sapiens.
XX PN WO200274979-A2.
XX PD 26-SEP-2002.
XX PF 20-MAR-2002; 2002WO-US008456.
XX PR 20-MAR-2001; 2001US-0276947P.
XX PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX PI Wan J, Wang Y;
XX DR WPI; 2002-740862/80.
XX PT New gene expression profile generated from primary, endothelial,
XX PT epithelial, and muscle cell types, useful for identifying disease
XX PT pathologies involving alterations of gene expression, e.g. cancer.
XX PS Example 3; Page 818-819; 850bp; English.

The invention relates to a gene expression profile comprising one or more genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type is a coronary artery endothelium, umbilical artery or vein endothelium, aortic endothelium, dermal microvascular endothelium, pulmonary artery endothelium, myometrium microvascular endothelium, keratinocyte endothelium, bronchial epithelium, mammary epithelium, prostate epithelium, renal cortical epithelium, renal proximal tubule epithelium, small airway epithelium, renal epithelium, umbilical artery smooth muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle, dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, aortic smooth muscle, mesangial cells, coronary artery smooth muscle, bronchial smooth muscle, uterine smooth muscle, lung fibroblast, osteoblasts or prostate stromal cell. The gene expression profile is used

for determining the level of RNA expression for a sample, determining the phenotype of a cell, and distinguishing cell types. The gene or a protein expression profile is useful in identifying disease pathologies involving alterations of gene expression. The assessment of expression profiles may provide meaningful information with respect to tumour type and stage, treatment methods, and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for genetic and physical mapping of genomes, DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antiviral or antifungal agents

Sequence 2135 BP; 537 A; 537 C; 482 G; 579 T; 0 U; 0 Other;

Query Match 95.2%; Score 1256.2; DB 6; Length 2135;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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OY 52 ACTGACCTCTGGGAGTCCCTTCCAGAGAGATGATCGGAGAGCAACCCGAGCTA 111
DB 242 ACTTCTTTAGGGAGAGTCCCTTCCAGAGAGATGATCGGAGAGCAACCCGAGCTA 301
OY 112 GTCCAGCAGACAGAGTGAACATTACAGATTTTACAAAGTCTCTCTGCTTCAAG 171
DB 302 GTCCAGCAGACAGAGTGAACATTACAGATTTTACAAAGTCTCTCTGCTTCAAG 361
OY 172 GAGATGAGAGAAATCCAGTGTGGGAGAACTTCATGACATGAGTGTTCATGTGC 231
DB 362 GAGATGAGAGAAATCCAGTGTGGGAGAACTTCATGACATGAGTGTTCATGTGC 421
OY 232 CTGAACCCAGCAGCAGCTGAGCATTCAGTCTGCTCCCTGAGGCACTTCAAG 291
DB 422 CTGAACCCAGCAGCAGCTGAGCATTCAGTCTGCTCCCTGAGGCACTTCAAG 481
OY 292 GTCTGAGAGAACTCTGAGTGTGCGTCACTCTCCAGAGCTCTGCTGAGG 351
DB 482 GTCTGAGAGAACTCTGAGTGTGCGTCACTCTCCAGAGCTCTGCTGAGG 541
OY 352 CCTTCTTACCACTTCAATGGGAGCTGTGGGAGAGCTCTGAGGAGTCAATTTT 411
DB 542 CCTTCTTACCACTTCAATGGGAGCTGTGGGAGAGCTCTGAGGAGTCAATTTT 601
OY 412 GTCTACAGCTTCAATGATTCACAGTGTTCACACGCAAGATAGCCGAACTGTTCTG 471
DB 602 GTCTACAGCTTCAATGATTCACAGTGTTCACACGCAAGATAGCCGAACTGTTCTG 661
OY 472 TTCAAACTGGGTGGGTCAAGGCTCTTCACTGCTCTGCTGAGGCAAGCTGTTCTCA 531
DB 662 TTCAAACTGGGTGGGTCAAGGCTCTTCACTGCTCTGCTGAGGCAAGCTGTTCTCA 721
OY 532 GCCATCGACAGGTACATATCCATTGACAGGCCCCCTGAGGCTATTAAGATTTGTCAACAG 591
DB 722 GCCATCGACAGGTACATATCCATTGACAGGCCCCCTGAGGCTATTAAGATTTGTCAACAG 781
OY 592 CCCAAGCCGTTGGTACGTTTTCCTGATGTGAACATAGCCATTGTGATCGCGTGTGCTG 651
DB 782 CCCAAGCCGTTGGTACGTTTTCCTGATGTGAACATAGCCATTGTGATCGCGTGTGCTG 841
OY 652 CCTCTCTGGGCTGGAATGCGAGAACTGCAATCTGTTGTCAAGACATTTTCCACAG 711
DB 842 CCTCTCTGGGCTGGAATGCGAGAACTGCAATCTGTTGTCAAGACATTTTCCACAG 901
OY 712 ATTGATGAACCTACCTGATGTGTTGGAATCGGGGTCAACAGGTACTGTTTCTGTTCAATC 771
DB 902 ATTGATGAACCTACCTGATGTGTTGGAATCGGGGTCAACAGGTACTGTTTCTGTTCAATC 961
OY 772 GTGTATGGGTACATGATATTTCTCTGGAAGGCTCAAGCCGCTCGCATGATTCAG 831
DB 962 GTGTATGGGTACATGATATTTCTCTGGAAGGCTCAAGCCGCTCGCATGATTCAG 1021
OY 832 CGTGCACCCAGAGAGCATCATTCACACGCTCTGAGATGGAGGTACAGGTGACC 891
DB 1022 CGTGCACCCAGAGAGCATCATTCACACGCTCTGAGATGGAGGTACAGGTGACC 1081
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OY 892 CGGCCAGACCAAGCCCGCATGAGCATTTAGTACCAAGACCTGTCCTGATCTGTG 951
DB 1082 CGGCCAGACCAAGCCCGCATGAGCATTTAGTACCAAGACCTGTCCTGATCTGTG 1141
OY 952 GTGTATGATCATCTGTGGGCTCTGTGCTGCAATCATGATGTATGATGTTCTTGGAG 1011
DB 1142 GTGTATGATCATCTGTGGGCTCTGTGCTGCAATCATGATGTATGATGTTCTTGGAG 1201
OY 1012 ATGAACAGCTCATTAAGACGCTGTTTGCATTTCTGCAATATGCTCTGCTGCACTCC 1071
DB 1202 ATGAACAGCTCATTAAGACGCTGTTTGCATTTCTGCAATATGCTCTGCTGCACTCC 1261
OY 1072 ACCGTAACCCCATCATATGATCTGAGAGATGAGACCTGAGACAGCTTTCGAGAC 1131
DB 1262 ACCGTAACCCCATCATATGATCTGAGAGATGAGACCTGAGACAGCTTTCGAGAC 1321
OY 1132 ATGTTTCCCTCTTGTGAAGGACATGCGAGGCTCTGTGATTAACAGATGGGGAATCGAG 1191
DB 1322 ATGTTTCCCTCTTGTGAAGGACATGCGAGGCTCTGTGATTAACAGATGGGGAATCGAG 1381
OY 1192 TGCTGCACAAAACGCAAAATGACAGCCAGTGTTCACAGGGCCGCAAAAGCTGATC 1251
DB 1382 TGCTGCACAAAACGCAAAATGACAGCCAGTGTTCACAGGGCCGCAAAAGCTGATC 1441
OY 1252 AAGAGCAGGTCAAGATTGCCAAGGTAAACATGCTGTGTCACAGACAGCTGCGGAG 1311
DB 1442 AAGAGCAGGTCAAGATTGCCAAGGTAAACATGCTGTGTCACAGACAGCTGCGGAG 1501
OY 1312 GCTCTGTGA 1320
DB 1502 GCTCTGTGA 1510
```

RESULT 15
ACAS6852
ID ACAS6852 standard; cDNA; 2135 BP.

ACAS6852;

06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1450.

Human; probe; ss; array element; Parkinson's disease;
signalling pathway population; cancer; adenocarcinoma; leukemia;
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

Homo sapiens.

US6500938-B1.

31-DEC-2002.

30-JAN-1998; 98US-00016434.

30-JAN-1998; 98US-00016434.

(INCY-) INCYTE GENOMICS INC.

Au-Young J, Seilhamer JJ;

WPI; 2003-352189/33.

Combination of polynucleotide probes, useful as array elements in a
microarray for monitoring the expression of a number of target
polynucleotides.

Claim 1; SEQ ID NO 1450; 65pp; English.

The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an

CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPRO at
CC begdata.uspto.gov/sequence.html?docID=06500938B1
CC
CC
XX

Sequence 2135 BP; 537 A; 537 C; 482 G; 579 T; 0 U; 0 Other;

Query Match 95.2%; Score 1256.2; DB 10; Length 2135;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

52 ACTGACCTCTCTGGAAGTCCCTTCCAGAGAAAGTATGCTGGGAGACACCCCGAGCTA 111
242 ACTTCTTTAGGGAGAGTCCCTTCCAGAGAAAGTATGCTGGGAGACACCCCGAGCTA 301
112 GTCCAGAGACAGAGTGAACATTAAGAAATTTTCAACAGTCTCTCGTCCCTTCAAG 171
302 GTCCAGAGACAGAGTGAACATTAAGAAATTTTCAACAGTCTCTCGTCCCTTCAAG 361
172 GAGAAATGAGAGAACATCCAGTGTGGGAGAACTTCATGAGATAGAGTTCATGATC 231
362 GAGAAATGAGAGAACATCCAGTGTGGGAGAACTTCATGAGATAGAGTTCATGATC 421
232 CTGAAACCCAGACAGAGTGGCCATTTGAGTCTCTCTCGTCCCTTCAAG 291
422 CTGAAACCCAGACAGAGTGGCCATTTGAGTCTCTCTCGTCCCTTCAAG 481
292 GTCCAGAGACAGAGTGAACATTAAGAAATTTTCAACAGTCTCTCGTCCCTTCAAG 351
482 GTCCAGAGACAGAGTGAACATTAAGAAATTTTCAACAGTCTCTCGTCCCTTCAAG 541
352 CTTTCTTCAACATTCATCGGCAAGCTTGGCGGTGGAGACCTCTGGGAGGTGTCAATTTT 411
542 CTTTCTTCAACATTCATCGGCAAGCTTGGCGGTGGAGACCTCTGGGAGGTGTCAATTTT 601
412 GTCTTACAGCTTATGATCTTCAAGGTGTTCACCGGAAAGATAGCCGCAACGTGTTCTG 471
602 GTCTTACAGCTTATGATCTTCAAGGTGTTCACCGGAAAGATAGCCGCAACGTGTTCTG 661
472 TTCAAAATGAGGAGGTGACAGGCTCTTCACTGCTCCGTGGGAGAGCTGTTCTTCA 531
662 TTCAAAATGAGGAGGTGACAGGCTCTTCACTGCTCCGTGGGAGAGCTGTTCTTCA 721
532 GCCATGCAAGGTATCATATTCATTCACAGGCTCTGCTATTAAGAGATGTCCACAG 591
722 GCCATGCAAGGTATCATATTCATTCACAGGCTCTGCTATTAAGAGATGTCCACAG 781
592 CCCAAGGCGGTGTGAGCTTTTGGCTGATGTGACCATAGCCATTGTGATGCGCGTCTG 651
782 CCCAAGGCGGTGTGAGCTTTTGGCTGATGTGACCATAGCCATTGTGATGCGCGTCTG 841
652 CCTCTCTGGGCTGGAATGCGAGAAATGCAATCTGTTTGTCTAGACATTTTCCACAC 711
842 CCTCTCTGGGCTGGAATGCGAGAAATGCAATCTGTTTGTCTAGACATTTTCCACAC 901
712 ATTGATGAACCTTACCTGATGTTCTGATTCGGGATCACCAGGTAATGCTTCTGTTCA 771
902 ATTGATGAACCTTACCTGATGTTCTGATTCGGGATCACCAGGTAATGCTTCTGTTCA 961

QY 772 GTGATGCTATCATGATATATTTCTTGAAGGCTCACAGCCCTCCGATGATTCAG 831
DB 962 GTGATGCTATCATGATATATTTCTTGAAGGCTCACAGCCCTCCGATGATTCAG 1021
QY 832 CGGACACCCAGAAAGGATCATATTCACAGGCTGAGAGATGGAGATGAGGATGAC 891
DB 1022 CGGACACCCAGAAAGGATCATATTCACAGGCTGAGAGATGGAGATGAGGATGAC 1081
QY 892 CGGACACCCAGAAAGGATCATATTCACAGGCTGAGAGATGGAGATGAGGATGAC 951
DB 1082 CGGACACCCAGAAAGGATCATATTCACAGGCTGAGAGATGGAGATGAGGATGAC 1141
QY 952 GTGATGATATCTGCTGGGCTCTCTGCTTGAATCATGATGATGATGATGATG 1011
DB 1142 GTGATGATATCTGCTGGGCTCTCTGCTTGAATCATGATGATGATGATGATG 1201
QY 1012 ATGAACAGGCTATTAAGACGAGTGTGATTCAGAGTATGATGATGATGATGATG 1071
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QY 1072 ACCGTAACCCCATCATATGCTCTGAGAGTAAAGACCTGCGACACGCTTCCGAG 1131
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QY 1132 ATGTTTCCCTCTTGAAGGCACTGCGACGCTCTGATTAACGATGGGGAATCGAG 1191
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QY 1192 TGCCGCAACAAACAGCAAAATGACAGGTGTTCAAGGCGCGAGAAAGCTGCAATC 1251
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QY 1252 AAGACACAGTCAAGATTGCAAGGTAAACATGCTGTGTCCACAGACAGCTCTGCGAG 1311
DB 1442 AAGACACAGTCAAGATTGCAAGGTAAACATGCTGTGTCCACAGACAGCTCTGCGAG 1501
QY 1312 GCTCTGTGA 1320
DB 1502 GCTCTGTGA 1510

Search completed: June 16, 2006, 23:47:30
Job time : 842 secs

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Db	151	ACTTCTTTAGGGAGATCCCTTCCAGAGAGATGATGCTGGGAGAGACACCCGAGCTA	210	
Oy	112	GTCCAGAGACACAGGTGAACATTAAGAAATTTTCAACAAGTCTCTCGTCTTCAAG	171	
Db	211	GTCCAGAGACACAGGTGAACATTAAGAAATTTTCAACAAGTCTCTCGTCTTCAAG	270	
Oy	172	GAGATGAGAGAAATCAAGTGGGAGAACTTCAAGACATGAGAGTTTCAAGTTC	231	
Db	271	GAGATGAGAGAAATCAAGTGGGAGAACTTCAAGACATGAGAGTTTCAAGTTC	330	
Oy	232	CTGAACCCGAGCAGCAGCTGGCCATTCAGTCTGCTCCAGCCTGGGACCTTCAAG	291	
Db	331	CTGAACCCGAGCAGCAGCTGGCCATTCAGTCTGCTCCAGCCTGGGACCTTCAAG	390	
Oy	292	GTCTGAGAGAACTTCTGGTGTGTGCGTCACTCTCCAGCCTCCGCTGCAAG	351	
Db	391	GTCTGAGAGAACTTCTGGTGTGTGCGTCACTCTCCAGCCTCCGCTGCAAG	450	
Oy	352	CCTTCTCACTTATGATGCGGACCTGGGCGTGGAGACCTCTGGGAGTGCATTTT	411	
Db	451	CCTTCTCACTTATGATGCGGACCTGGGCGTGGAGACCTCTGGGAGTGCATTTT	510	
Oy	412	GTCTACAGCTTCACTTCAAGTGTTCACCGCAAGATAGCCGCAAGCTGTTCG	471	
Db	511	GTCTACAGCTTCACTTCAAGTGTTCACCGCAAGATAGCCGCAAGCTGTTCG	570	
Oy	472	TTCAACAGTGGGTGAGTCAAGGCTCTTCACTGCTCCGTGGGACCTGTTCCTACA	531	
Db	571	TTCAACAGTGGGTGAGTCAAGGCTCTTCACTGCTCCGTGGGACCTGTTCCTACA	630	
Oy	532	GCCATGACAGGTATATATCCATTCACAGGCCCCCTGACCTATAGAGATTGTCACAG	591	
Db	631	GCCATGACAGGTATATATCCATTCACAGGCCCCCTGACCTATAGAGATTGTCACAG	690	
Oy	592	CCCAAGGCGGTGAGCTTTTCCGTGATGAGACCATAGCCATTGTGTCGCTG	651	
Db	691	CCCAAGGCGGTGAGCTTTTCCGTGATGAGACCATAGCCATTGTGTCGCTG	750	
Oy	652	CCTTCTCTGGGTGAGTCTGCAAGAACTGCAATCTGTTGCTCAGACATTTTCCACAC	711	
Db	751	CCTTCTCTGGGTGAGTCTGCAAGAACTGCAATCTGTTGCTCAGACATTTTCCACAC	810	
Oy	712	ATTGATGAACCTACCTGATGTTTCTGGATCGGGGTCAACAGGATCTGCTGTTCAATC	771	
Db	811	ATTGATGAACCTACCTGATGTTTCTGGATCGGGGTCAACAGGATCTGCTGTTCAATC	870	
Oy	772	GTGTATGCGTACATGATATATCTCTGGAAGGCTCACAGCCGCTCCGACATGATTCAG	831	
Db	871	GTGTATGCGTACATGATATATCTCTGGAAGGCTCACAGCCGCTCCGACATGATTCAG	930	
Oy	832	CGTGGACCCAGAGAGACATCATCATCAAGCTGAGAGATGGAGGTAACAAGTAC	891	
Db	931	CGTGGACCCAGAGAGACATCATCATCAAGCTGAGAGATGGAGGTAACAAGTAC	990	
Oy	892	CGGCGACAGCAAGCCCGCATGAGCATTTAGGTAAGCAACCTGATCTGATCCGAGT	951	
Db	991	CGGCGACAGCAAGCCCGCATGAGCATTTAGGTAAGCAACCTGATCTGATCCGAGT	1050	
Oy	952	GTGTGATCATCTGCTGGGCGCTCTGCTTGCATCATGATGATGATGATCTTTGGAG	1011	
Db	1051	GTGTGATCATCTGCTGGGCGCTCTGCTTGCATCATGATGATGATGATCTTTGGAG	1110	
Oy	1012	ATGAACAAGCTCATTAAGACGCTGTTGCAATCTGCAAGATGCTGCTGCTGAACTCC	1071	
Db	1111	ATGAACAAGCTCATTAAGACGCTGTTGCAATCTGCAAGATGCTGCTGCTGAACTCC	1170	
Oy	1072	ACCGTGAACCCCATATATATGCTCTGAAGAGTAAGACCTGGAACAGCTTTCCGAGC	1131	

Db	1171	ACCGTGAACCCCATCATATGCTCTGAGAGTAAGACCTGGACACGCTTTCGGAGC	1230	
Oy	1132	ATGTTTCCCTTGTGAAAGCACTGCGCAGCTCTGATTAACAGATGGGGGAACTCGGAC	1191	
Db	1231	ATGTTTCCCTTGTGAAAGCACTGCGCAGCTCTGATTAACAGATGGGGGAACTCGGAC	1290	
Oy	1192	TGCGTGAACAAACGCAACAAATGACGCGAGTGTCAAGGCGCGAGAAAGTGCATC	1251	
Db	1291	TGCGTGAACAAACGCAACAAATGACGCGAGTGTCAAGGCGCGAGAAAGTGCATC	1350	
Oy	1252	AAGACAGGTCAAGATTGCCAAGTAAACATGCTGTGTTCACAGACACGCTGCGAG	1311	
Db	1351	AAGACAGGTCAAGATTGCCAAGTAAACATGCTGTGTTCACAGACACGCTGCGAG	1410	
Oy	1312	GCTCTGTGA 1320		
Db	1411	GCTCTGTGA 1419		
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DEFINITION				Mus musculus CNR1 gene, VIRUTAL TRANSCRIPT, partial sequence,
ACCESSION				AY415604
VERSION				AY415604.1 GI:39771563
KEYWORDS				GSS.
SOURCE				Mus musculus (house mouse)
ORGANISM				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Muridae; Mus.
REFERENCE				1 (bases 1 to 1422)
AUTHORS				Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE				Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL				Science 302 (5652), 1960-1963 (2003)
PUBMED				14671302
REFERENCE				2 (bases 1 to 1422)
AUTHORS				Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE				Direct Submission
JOURNAL				Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT				This sequence was made by sequencing genomic exons and ordering them based on alignment.
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gene				/organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1..>1422 /gene="CNR1" /locus_tag="HCM5612"
ORIGIN				
Query Match		79.4%;	Score 1048;	DB 14; Length 1422;
Best Local Similarity		89.5%;	Pred. No. 1.9e-262;	
Matches 1139;		Conservative	0; Mismatches 130;	Indels 3; Gaps 1;
Oy	52	ACTGACCTCTGGGAAGTCCCTTCCAAAGAGAATGATCGGGGAGACCAACCCGACGTA	111	
Db	151	ACTTCCTTCAAGGGGTAAGTCCCTTCCAAAGAGAATGATCGGGGAGACCAACTCCCGTTG	210	
Oy	112	GTCCAGC---AGACAGGTGAACATTCAGAAATTTTCAACAACAATCTCTCGTCTCTC	168	
Oy	211	GTTCACAGAGGAGACCAACCAACTTACAGAGTTCTATACAAATCTCTCATACGTTTC	270	

QY	169	AAGGAGATGAGAGAAACATCCAGTGTGGGGAGAACTTCATGACATTAAGTGTTCATG	228
Db	271	AAGGAGAAAGAGAGACAAATCCAGTGTGGGGAGAAATTTTATGACATTAAGTGTTCATG	330
QY	229	GTCCTGAACCCAGCCAGAGCTGGGCAATTGAGTCTCTCTCCCTCAACGCTGGGCACTTC	288
Db	331	ATTCTGAATCCAGCCAGAGAGCTGGGCAATCGTGTCTCTCTCACTGGGCACTTC	390
QY	289	ACGGTCTTGAGAACCTCTCTGGTGTGTGCTGATCTCCACTCCGCAAGCCTCCGCTGC	348
Db	391	ACGGTCTTGAGAAACCTCGTGGTGTGATGTGATCTCTCACTCCGCAAGTCTCCGATGC	450
QY	349	AGGCTTCCTACCACTTCAATGGGAGCCCTGGGGGTGGAGACCTCCTGGGAGTGTCAAT	408
Db	451	AGGCTTCCTACCACTTCAATGGGAGCCCTGGGGGTGGAGACCTCCTGGGAGTGTCAAT	510
QY	409	TTTGTCTACAGCTTCATTTGACTTCCACGTGTCCACCCGAAAGATAGCCGCAACGTGTT	468
Db	511	TTTGTCTACAGCTTTTGTGTGACTTTCACCGTGTTCACCCGAAAGATAGTCCCAATGTGTT	570
QY	469	CTGTTCAAACTGGGTGGGGGTCAACGGCTCTCTTCACTGCTCCGTGGGCAAGCTGTCTTC	528
Db	571	CTGTTCAAACTGGGTGGGGGTTCACGGCTCTTTCACAGCACTGTGTGGGCAAGCTGTCTTC	630
QY	529	ACAGGCATCGACAGGTAATATTCACATTCACAGGCCCTGGGCCCTAATPAAGAGATTGCAAC	588
Db	631	ACGGCCATCGACAGGTAATATTCACATTCACAGGCCCTGGGCCCTAATPAAGAGATTGCAAC	690
QY	589	AGGCCCAAGGCCGTGTAGCGTTTTGTGCTGATGTGACCATAGCAATTGTGATTCGCCGTG	648
Db	691	AGGCCCAAGGCCGTGTAGCGCTTTTGTGCTGATGTGACCATAGTAATTGTGCTGTG	750
QY	649	CTGCCCTCTCCCTGGGGCTGGAACTGGCAGAACTGGCAATCTGTTTGTCTCAGACATTTTCCCA	708
Db	751	TTGCTCTCTCCTGGGGCTGGAACTGGCAGAACTGGCAATCTGTTTGTCTCAGACATTTTCCCA	810
QY	709	CACATTGATGAACCTTAACCTGATGTTCGTGGATCGGGGGTCAACAGCGTACTGCTCTGTTC	768
Db	811	CTCAATTGATGAACCTTAACCTGATGTTCGTGGATCGGGGGTCAACAGCGTACTGCTCTGTTC	870
QY	769	ATCGGTATATGCGTACATGTATATTTCTCTGGAAAGGCTCACAGCCAGCCGTCCGATGATT	828
Db	871	ATTGTGATATGCGTACATGTATATTTCTCTGGAAAGGCTCACAGCCAGCCGTCCGATGATT	930
QY	829	CAGCGTGGACCCAGAGAAGCATATCATCCACAGTCTGAAGATGGGAAGGTACAGGTG	888
Db	931	CAGCGTGGAAACCCAGAAAAGCATATCATCTCACACTCAGAAAAGATGGCAAGGTGAGGTG	990
QY	889	ACCCGGCCAGAACCAAGCCCGCAGTGAATTAAGTTAGCCAGCAAGCCCTGTCTCTGAATCTG	948
Db	991	ACAGCGGCTGACCAAGCCCGCAGTGAATTAAGTTAGCTGGCCAAAACCTGGTCTGTGATCTG	1050
QY	949	GTCGTGTGTGATCATTTGCTGGGGCCCTCTGCTTTCGATATCATAGGTGTATATGTCTTTGGG	1008
Db	1051	GTCGTGTGTGATCATTTGCTGGGGCCCTCTGCTTTCGATCATAGGTGTATATGTCTTTGGG	1110
QY	1009	AAGATGAACAAGCTCATTTAAGACGGGTGTGATTTCTGCAATATCTCTGCTGCTGAAC	1068
Db	1111	AAGATGAACAAGCTTATATCAAGACGGGTGTGATTTCTGCAATATCTCTGCTGCTGAAC	1170
QY	1069	TCACCGTGAACCCCATCATCTATGCTCTGAGAGATTAAAGCACTGCGACACGCTTTCCGG	1128
Db	1171	TCACCGTGAACCCCATCATCTATGCTCTGAGAGATTAAAGCACTGAGCATCTTTCCGGC	1230
QY	1129	AGCATGTTTCCCTCTTGTGAAGAGCACTGGGCAAGCCCTGGAATPAACAGCATGGGGGACCTG	1188
Db	1231	AGCATGTTTCCCTTATGTGAAGAGCACTGGGCAAGCCCTCTAAGATPAACAGCATGGGGGACCTCA	1290
QY	1189	GACTGCTTCGACAAACAGGCAAAACAATGACGCAAGTGTTCACAGGGCCGCAAGAAAGCTGC	1248
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QY	1249	ATCAAGACACAGGCTCAACATTTGGCAAGTACCAATGCTGTGTCACAGACGCTGCC	1308
Db	1351	ATCAAGACACACTGTTAAGATGCGCAAGGTACCAATGCTGTGTCACAGACGCTGCC	1410
QY	1309	GAGGCTCTGTGA	1320
Db	1411	GAGGCTCTGTGA	1422
RESULT 3			
LOCUS	AK139417		
DEFINITION	AK139417	1642 bp	linear
ACCESSION	AK139417		
VERSION	AK139417.1		
KEYWORDS	HTC, CAP trapper.		
SOURCE	Mus musculus		
ORGANISM	Mus musculus (house mouse)		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohmori, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	11076861		
REFERENCE			
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, T., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Caasavart, T., Fleischmann, W., Gaasterland, T., Gissi, C., Kling, B., Kohtawa, H., Kusih, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staahl, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, D., Boffelli, D., Bojunga, N., Carinacci, P., de Bonaldo, M. F., Brownstein, M. J., Ball, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Rung, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Saeki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-Oka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Sorts, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohyaku, S., and Hayashizaki, Y.		
CONSTRM	RIKEN Genome Exploration Research Group Phase II Team and the		
TITLE	PANTOM Consortium		
JOURNAL	Functional annotation of a full-length mouse cDNA collection		
PUBMED	Nature 409 (6821), 685-690 (2001)		
REFERENCE	11217851		

AUTHORS	CONSRMT TITLE	JOURNAL PUBMED REFERENCE AUTHORS
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Ooto, N., Saito, R., Suzuki, H., Yamataka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schmitt, L.M., Kanapin, A., Matsuda, H., Bernalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Glasi, C., Godzik, A., Gough, J., Grimmond, S., Guenichon, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mik, H., Nagashima, T., Munata, K., Okido, T., Pavan, W.J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, J.C., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12466851	PANTOM Consortium
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Ooto, N., Saito, R., Suzuki, H., Yamataka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schmitt, L.M., Kanapin, A., Matsuda, H., Bernalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Glasi, C., Godzik, A., Gough, J., Grimmond, S., Guenichon, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mik, H., Nagashima, T., Munata, K., Okido, T., Pavan, W.J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, J.C., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12466851	PANTOM Consortium

REFERENCE AUTHORS	PUBMED 16141072	CONSRMT TITLE	JOURNAL PUBMED REFERENCE AUTHORS
Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yagi, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Matlick, J., Hume, D.A., Lipovich, L., Bernalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlstedt, C.	RIKEN Genome Exploration Research Group Antisense transcription in the mammalian transcriptome Science 309 (5740), 1564-1566 (2005) 16141073	8 (bases 1 to 1642) Arkawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanishi, A., Muramatsu, M. and Hayashizaki, Y.	Direct Submission Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers		
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RESULT 4
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DEFINITION Pan troglodytes CNR1 gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESSION AY415603
VERSION AY415603.1 GI:3971562
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
REFERENCE 1 (bases 1 to 821)
Clark A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 821)
Clark A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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location/Qualifiers
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Best Local Similarity 98.2%; Pred. No. 9.4e-199;
Matches 806; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 182 AGAATATCAATGAGGAGAACTTCAATGAGATGTTTCAATGCTCCGAAACCCCA 241
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QY 302 ACTTCCTGCTGTGCTGATCTCTCACTCCGAGCTTCGCTGACAGGCTTCTTACC 361
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Qy 482 GTGGGGTACGAGCGCTCTTCACTGCTCGTGGGAGCGCTGTTCTTCAACAGCATGACA 541
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RESULT 5
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LOCUS DEFINITION 1361255 MARC 7BOV Bos taurus CDNA 5', mRNA sequence.
ACCESSION DN533141
VERSION DN533141.1 GI:60981254
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Peccora; Bovidae; Bovinae; Bos.
1 (bases 1 to 769)
Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-Mckown,C.G.,
Wray,J.B. and Keefe,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPJ
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
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Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLR8056 row: D column: 11
Seq primer: GTAATACGACCTCACTATTAAGG.
Location/Qualifiers
1. 769
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/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_id="MARC 7BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN
Query Match 48.5%; Score 639.8; DB 9; Length 769;
Best Local Similarity 91.6%; Pred. No. 9.1e-156;
Matches 677; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 247 CAGCTGGCCATTGCAAGTCTTCTCTCAAGCTGGGACCTTCAAGGTCCTGAGAACTTC 306
Db 1 CAGCTGGCCATTGCAAGTCTTCTCTCAAGCTGGGACCTTCAAGGTCCTGAGAACTTC 60
Qy 307 CTGGTGTGTCGCTCATCTCCATCCCGAGCCCTCGCTGAGAGCCCTTCACTTC 366
Db 61 CTGGTGTGTCGCTCATCTCCATCCCGAGCCCTCGCTGAGAGCCCTTCACTTC 120
Qy 367 ATCGGACGCTGGCGGATGAGACCTCTGAGGAGTGCATTTTGTCTACAGCTTCAT 426
Db 121 ATCGGACGCTGGCGGATGAGACCTCTGAGGAGTGCATTTTGTCTACAGCTTC 180
Qy 427 GACTTCACGCTGTTCCACCGCAAGATAGCCGCAAGCTGTTTCTGTTCAAACTGGGTGG 486
Db 181 GACTTCACGCTGTTCCACCGCAAGATAGCCGCAAGCTGTTTCTGTTCAAACTGGGTGG 240
Qy 487 GTCAAGGCTCTTCACTGCGCTCGTGGGAGCCGTTCTCAAGACCATGACAGTAC 546
Db 241 GTCAAGGCTCTTCACTGCGCTCGTGGGAGCCCTGTTCTCAAGACCATGACAGTAC 300
Qy 547 ATATTCATTCAAGGCGCCCTGACTATAGAGATTTGTCAACAGGCCCAAGCCGTGTGA 606
Db 301 ATATTCATTCAAGGCGCCCTGACTATAGAGATTTGTCAACAGGCCCAAGCCGTGTGA 360
Qy 607 GCGTTTTCCTGATGTGACCAATGACCATTTGATGCGCGTGTCTCTCTGGGCTGG 666
Db 361 GCGTTTTCCTGATGTGACCAATGACCATTTGATGCGCGTGTCTCTCTGGGCTGG 420
Qy 667 AATCGGAGAAATCGCATATGTTTGTCTCAGACATTTCCACACATTTGATGAACCTAC 726
Db 421 AATCGGAGAAATCGCATATGTTTGTCTCAGACATTTTCCCTCTATGAGACACCTAC 480
Qy 727 CTGATGTTCTGGATCGGGGTACACGCTACTGCTTCTGTTCACTGATGATGCTACATG 786
Db 481 CTGATGTTCTGGATCGGGGTACACGCTACTGCTTCTGTTCACTGATGATGCTACATG 540
Qy 787 TATATTTCTGGAAGCTTCAAGCCACGCGTCCGATGATTCAGCGTGGACCCAGAG 846
Db 541 TATATTTCTGGAAGCTTCAAGCCACGCGTCCGATGATTCAGCGTGGACCCAGAG 600
Qy 847 AGCATCATATCCACAGCTCGAGGATGGAGAGTGAAGCCGCGCAGACCAAGCC 906
Db 601 AGCATCATATCCACAGCTCGAGGATGGAGAGTGAAGCCGCGCAGACCAAGCC 660
Qy 907 CGCATGACATTTAGGTTAGCAAGACCTGTGCTGATCTGTGTTGATATCTGTC 966
Db 661 CGCATGACATTTAGGTTAGCAAGACCTGTGCTGATCTGTGTTGATATCTGTC 720
Qy 967 TGGGGCGCTTGTGTTCAA 985
Db 721 TGGGGCGCTTGTGTTCAA 739

RESULT 6
CA327850 752 bp mRNA linear EST 09-JUL-2003
LOCUS DEFINITION UI-M-PYO-cw-f-15-0-UI.r1 NIH_BMAP_PYO Mus musculus CDNA clone
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IMAGE:6825328 5', mRNA sequence.
ACCESSION CA327850
VERSION CA327850.1 GI:24545948
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 752)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
source

Location/Qualifiers
1..752
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6825328"
/issue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP PY0"
/note="Organ: Brain; Vector: pYX-Abc; Site 1: Bcor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Bcor I adaptor, digested with NotI and then cloned
directionally into pYX-Abc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
Program coordinator."

ORIGIN

Query Match 48.0%; Score 634.2; DB 4; Length 752;
Best Local Similarity 90.2%; Pred. No. 2.6e-154;
Matches 678; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 394 CTGGGAGTGCATTTTGTCTACAGCTTCACTTCACGTTTCACCGCAAGAT 453
DB 1 CTGGGAGTGCATTTTGTCTACAGCTTGTGACTTCACGTTTCACCGCAAGAT 60
QY 454 AGCGGACGCTTCTGTCAAACTGGGTGGGCTCAGCGGCTCTTCACTGCTCCGTG 513
DB 61 AGTCCCAATGTTTCTGTCAAACTGGGTGGGCTCAGCGGCTCTTCACTGCTCCGTG 120
QY 514 GCGAGCTTCTCTCAGACCATCAGAGTACATATCATTCACAGGCCCCCTGACCTAT 573
DB 121 GCGAGCTTCTCTCAGACCATCAGAGTACATATCATTCACAGGCCCCCTGACCTAT 180
QY 574 AAGAGATTTTCACAGGCCCCAAGGCGTGTAGCGTTTGCCTGATGTGACCAATGCC 633
DB 181 AAGAGATTTTCACAGGCCCCAAGGCGTGTAGCGTTTGCCTGATGTGACCAATGCC 240

QY 634 ATTGTGATGCGCGGTGCTGCTCTCTCGGCTGGAACTGGAGAACTGATCTGTTTC 693
DB 241 ATAGTATATGCTGTGTGCTCTCTCGGCTGGAACTGGAGAACTGATCTGTTTC 300
QY 694 TCAGACATTTTCCACACATGATGAAACCTTACCTGATTTTCTGATCGGGGTACACAC 753
DB 301 TCAGACATTTTCCACACATGATGAAACCTTACCTGATTTTCTGATCGGGGTACACAC 360
QY 754 GTACTGCTTCTGTTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 813
DB 361 GTACTGCTTCTGTTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 814 GCGTCCGATGATTTTCAAGGTGGACCCAGAGACATGATGATGATGATGATGATGAT 873
DB 421 GCGTCCGATGATTTTCAAGGTGGACCCAGAGACATGATGATGATGATGATGATGAT 480
QY 874 GGAAGGTATCAGGTGACCCGACAGCCGACAGCCGACAGCCGACAGCCGACAGCCG 933
DB 481 GGAAGGTATCAGGTGACCCGACAGCCGACAGCCGACAGCCGACAGCCGACAGCCG 540
QY 934 CTGCTCTGATCTGT 993
DB 541 CTGCTCTGATCTGT 600
QY 994 TATGATGCTTTTGGGAAATGAAACAGCTCATTAAGACGGTGTTCATTTGCACTATG 1053
DB 601 TATGATGCTTTTGGGAAATGAAACAGCTCATTAAGACGGTGTTCATTTGCACTATG 660
QY 1054 CTCTCCCTGCTGAACTTCACAGCCGTAACCCCATCATCTATGCTCTGAGGAGTAAGACCTG 1113
DB 661 CTCTCCCTGCTGAACTTCACAGCCGTAACCCCATCATCTATGCTCTGAGGAGTAAGACCTG 720
QY 1114 GCACAGCTTTTCGAGGAGATGTTTCCCTCTTG 1145
DB 721 AGACATGCTTTCCGACGATGTTCCCTTCAG 752

RESULT 7
LOCUS CA328435 737 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FY0-cdb-f-10-0-UI-r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE:6827243 5', mRNA sequence.
ACCESSION CA328435
VERSION CA328435.1 GI:24546533
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 737)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
source

Location/Qualifiers
1..737
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6827243"

/tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGCGAGACG. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 47.8%; Score 630.4; DB 4; Length 737;

Best Local Similarity 90.9%; Pred. No. 2.6e-153;

Matches 670; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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QY 414 CTACAGCTTCATTGACCTTCACGCTGTTCCACGCAAGATAGCCGGAAGCTGTTCTGTT 473
DB 1 CTACAGCTTCATTGACCTTCACGCTGTTCCACGCAAGATAGCTCCCAATGTTCTGTT 60
QY 474 CAACCTGGGAGGAGTCAAGGCTCTCTTCACTGCTCCGAGGAGCTGTTCTTCAACAGC 533
DB 61 CAACCTGGGAGGAGTCAAGGCTCTCTTCACTGCTCCGAGGAGCTGTTCTTCAACAGC 120
QY 534 CATGCAAGGTTCATATTCATTCACAGGCTCTGAGCTTAAAGAGATTTGACCAAGCC 593
DB 121 CATGCAAGGTTCATATTCATTCACAGGCTCTGAGCTTAAAGAGATTTGACCAAGCC 180
QY 594 CAAGGCGGTGAGGCTTTGCTGATGAGCACTAGGCAATGATGAGCGGTGCTGTC 653
DB 101 CAAGGCGGTGAGGCTTTGCTGATGAGCACTAGGCAATGATGAGCGGTGCTGTC 240
QY 654 TCTCTGGGCTGGAACCTGAGAGAACTGCAATCTGTTGCTGCAATTTTCCACACAT 713
DB 241 TCTCTGGGCTGGAACCTGAGAGAACTGCAATCTGTTGCTGCAATTTTCCACACAT 300
QY 714 TGATGAAACCTACCTGATGTTCTGAGATGAGGCTCACAGGCTACCTGCTTCTGATGCT 773
DB 301 TGATGAAACCTACCTGATGTTCTGAGATGAGGCTCACAGGCTACCTGCTTCTGATGCT 360
QY 774 GTATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833
DB 361 GTATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 834 TGGCAACCCGAGAGAGATCATCATCATCATCATCATCATCATCATCATCATCATCAT 893
DB 421 TGGCAACCCGAGAGAGATCATCATCATCATCATCATCATCATCATCATCATCATCAT 480
QY 894 GCGCAACCAAGGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 953
DB 481 GCGCAACCAAGGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 954 GTTGTATCATCTGCTGGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1013
DB 541 GTTGTATCATCTGCTGGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 1014 GAAACAAGCTCATTAAGACGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1073
DB 601 GAAACAAGCTCATTAAGACGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 660
QY 1074 CGTGAACCCCATCATCTATGCTGAGAGGAGCAAGGACTGAGACATGCTTTCGAGACAT 1133
DB 661 CGTGAACCCCATCATCTATGCTGAGAGGAGCAAGGACTGAGACATGCTTTCGAGACAT 720

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QY 1134 GTTCCCTCTGTGAGAG 1150
 DB 721 GTTCCCTCTGTGAGAG 737

RESULT 8
 LOCUS DY320503
 DEFINITION DY320503 717 bp. mRNA linear. EST 08-FEB-2006
 AGENCOURT 66892761 NIH_MGC_365 Rattus norvegicus cDNA clone
 IMAGE:8362287 5', mRNA sequence.

ACCESSION DY320503
 VERSION DY320503
 KEYWORDS DY320503.1 GI:87003257

SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murineae; Rattus.

REFERENCE 1 (bases 1 to 717)
 NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)

JOURNAL Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute

Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Howard J. Jacob

cDNA Library Preparation: Express Genomics
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLNL8153 row: n column: 13
 High quality sequence stop: 648.

Location/Qualifiers
 1..717

FEATURES

source

/organism="Rattus norvegicus"
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/db_xref="taxon:10116"
 /clone="IMAGE:8362287"

/tissue_type="whole brain, pool of 7"
 /lab_host="DH10B Tona"

/clone_lib="NIH MGC 365"

/note="Organ: brain/CNS; Vector: pExpress-1; Site 1:
 EcoRV; Site 2: NotI; cDNA was primed using oligo-dT
 primer: 5'-pGACTGATCTTACATGCGGCGGCGCC(7)25-3' and
 cloned into the EcoRV/NotI sites of pExpress-1.

Size-selection >1.3kb resulted in an average insert size
 of 2.0kb. This is a non-normalized primary library
 (normalized primary library is NIH_MGC_366) and was
 constructed by Express Genomics (Frederick, MD) for the
 Mammalian Gene Collection http://mgc.nci.nih.gov/."

ORIGIN

Query Match 46.7%; Score 616.2; DB 10; Length 717;

Best Local Similarity 91.2%; Pred. No. 1.3e-149;

Matches 654; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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DB 61 TTCTCACAAGCATGACAGGTATCATTTACAGAGGCTCTGAGCTATTAAGGATT 120
QY 583 GTCAACGAGGCGGAGGCGGTGATGAGGCTTTGCGGATGAGGACATATGACATTGTGATC 642
DB 121 GTCAACGAGGCGGAGGCGGTGATGAGGCTTTGCGGATGAGGACATATGATATC 180
QY 643 GCGGTGCTGCTCTCTGAGGCTGGAACCTGCAAGAACTGCAATCTGTTGCTCAGACATT 702

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Db 181 GCGTGTGCTCTCTCCGGGCTGMACTGMAAGCTGMACTGTCTTCTCTGGACATT 240
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Db 241 TTCCCACTCATTTACAGACCTTACTGATGTTCTGATGTTGGGTGACAGATGCTGCTG 300
QY 763 CTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 822
Db 301 CTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 823 ATGATTCAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 882
Db 361 ATGATTCAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 883 CAGGTGACCGGCTGACAGCAAGCCGCTGATGATGATGATGATGATGATGATGATG 942
Db 421 CAGGTGACCGGCTGACAGCAAGCCGCTGATGATGATGATGATGATGATGATGATG 480
QY 943 ATCTGTTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1002
Db 481 ATCTGTTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 1003 TTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1062
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QY 1063 CTGAATCCACCGTGAACCCCATGATGATGATGATGATGATGATGATGATGATG 1122
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QY 1123 TTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1179
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RESULT 9
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LOCUS
DEFINITION UI-M-FY0-cdr-m-10-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE:683555 5', mRNA sequence.
CB244710
CB244710.1 GI:28366354
EST
SOURCE
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurionathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 844)
NIH-MGC http://mgi.mgi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaab@nigms.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
source
Seq primer: pyx-5.
Location/Qualifiers
1..844
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:683555"
/tissue_type="whole brain"

/dev_stage="embryo 13.5,14.5,15.17,5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_11b="NIH BMAP_FY0"
/note="Organ: Brain; Vector: pyx-Anc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with Not I and then cloned
directionally into pyx-Anc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGCAGC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 45.7%; Score 602.8; DB 4; Length 844;
Best Local Similarity 90.6%; Pred. No. 4.4e-146;
Matches 665; Conservative 0; Mismatches 67; Indels 2; Gaps 2;
QY 285 CTTACGCTGCTGAGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 344
Db 1 CTTACGCTGCTGAGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 345 CTGAGGCTGCTGAGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 404
Db 61 ATGAGGCTGCTGAGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 405 CATTTTGTCTACAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 464
Db 121 CATTTTGTCTACAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 180
QY 465 GTTTCGTCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
Db 181 GTTTCGTCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 525 CCTCAGCAGTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 584
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QY 645 CGTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 704
Db 361 TGTGTTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 705 CCCACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 764
Db 421 CCCACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 765 GTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 824
Db 481 GTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 825 GATTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884
Db 541 GATTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 885 GGTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
Db 601 GGTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
QY 945 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
Db 660 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
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DB 719 TGGGAAGATGAACA 732

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RESULT 10
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LOCUS
DEFINITION UI-M-FX0-998-F-20-0-UI-r1 NIH BMAP_FX0 Mus musculus cDNA clone
IMAGE:30361963 5', mRNA sequence.
CF533059
ACCESSION
VERSION CF533059.1 GI:34585027
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciuromorphi; Muroidae; Muridae; Murinae; Mus.
REFERENCE
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution Information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pyx-5.
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
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/clone_1ib="NIH BMAP FX0"
/note="Organ: Brain; Vector: pyx-Anc; Site 1: Ecor I;
Site 2: Not I. The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pyx-Anc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

ORIGIN
Query Match 45.4%; Score 599.8; DB 5; Length 737;
Best Local Similarity 89.1%; Pred. No. 2.6e-145;
Matches 657; Conservative 0; Mismatches 79; Indels 1; Gaps 1;

QY 148 AACAACTCTCTCGTCTTCAAGGAATGAGAGACATCACTGT-GGGAGAACTT 206
|||||
DB 1 AACAGTCTCTCTCACTGTTCAAGGAGAGAGCAACATCCAGTGTGGGAGAACTT 60
|||||
QY 207 CATGACATAGAGTGTTCATGCTCTGAACCCAGCCAGGCTGGGCAATTGACGCT 266
|||||
DB 61 TATGACATAGAGTGTTCATGATTTGAAATCCAGCCAGGCTGGGCAATTGACGCT 120
|||||
QY 267 GTCCCTCAAGCTGGGCACTTCAAGGCTCTGAGAGAACTCTGTGTGCTCATCTCT 326
|||||

DB 121 GTCCCTCAAGCTGGGCACTTCAAGGCTCTGAGAGAACTGTGTGCTAATGTCTATCT 180
|||||

QY 327 CCATCTCCCGAGAGCTCCGCTGACAGGCTTCTTACCACTTATAGGAGAGCTGGGGTGGC 386
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DB 181 TCATCTCCCGAGAGTCTCCGATGACAGGCTTCTTACCACTTATAGGAGAGCTGGGGTGGC 240
|||||

QY 387 AGACCTCCGAGAGAGTGCATTTTGTCTACAGCTTCACTTCACTGATTCACAGC 446
|||||

DB 241 CGATCTCTGGGAAGTGCATCTTGTCTACAGCTTGTGTGATCTTCAAGGCTTCAAGC 300
|||||

QY 447 CAAGATAGCCGCAAGCTGTTCTGTTCAACCTGGTGGGTCAAGGCTTCTTCACTGC 506
|||||

DB 301 CAAGATAGTCCCAATGATGTTCTGTTCAAACTGGGTGGGTACCCGCTTCTTCAAGC 360
|||||

QY 507 CTCCGTGGGAGAGCTGTTCTTCCACAGGCACTGAGAGTATACCACTTCAAGGCTT 566
|||||

DB 361 ATCTGTGGGAGAGCTGTTCTTCCACAGGCACTGAGAGTATACCACTTCAAGGCTT 420
|||||

QY 567 GGCCCTATPAGAGATTTGATCAGAGCCCAAGGCGGTGAGCGTTTGGCTGATGTGAGC 626
|||||

DB 421 GGCTTATPAGAGATTTGATCAGAGCCCAAGGCGGTGAGCGTTTGGCTGATGTGAGC 480
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QY 627 CATAGCCATTTGTGATTCGCGTGTCTCTCTCTGAGGCTGGAAGCTGCAAGAACTGCAATC 686
|||||

DB 481 TATGCAATAGTAAATTTGCTGTGTTGCTCTCTCTGAGGCTGGAAGCTGCAATC 540
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QY 687 TGTTCGTCACAGATTTTCCACAGATGAGAACTTACCTGATGTTTGGAGATGGGGGT 746
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DB 541 TGTTCGTCACAGATTTTCCACAGATGAGAACTTACCTGATGTTTGGAGATGGGGGT 600
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QY 747 CACGAGCTACTGCTTCTGTTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 806
|||||

DB 601 CACGAGCTACTGTTGCTGTTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 660
|||||

QY 807 CAGCCAGCGCTGCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866
|||||

DB 661 CAGCCAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
|||||

QY 867 TGAGATGGGGAAGGTAC 883
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DB 721 CAGGATGGCAAGGTGC 737
|||||

RESULT 11
CO959553/C 774 bp mRNA linear EST 17-AUG-2004
LOCUS
DEFINITION AGENCOURT 30842409 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389731 3', mRNA sequence.
CO959553
ACCESSION
VERSION CO959553.1 GI:51324126
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMDI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMDI at:
<http://image.llnl.gov>

Plate: IRB17 row: e column: 09
High quality sequence start: 125
High quality sequence stop: 607.
Location/Qualifiers

FEATURES

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/clone_lib="NIH_MGC_146"
/notes="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image.rearrayed_plates/IRBF.presv.dat
a. Note: this is a NIH_MGC library."
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ORIGIN

Query Match 44.9%; Score 592.2; DB 8; Length 774;
Best Local Similarity 99.0%; Pred. No. 2.6e-143;
Matches 616; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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QY 690 TTGCTCAGACATTTTCCACACATTGATGAACCTGAGTTCTGATCGGGGTAC 749
DB 643 TTGTTCCAGACATTTTCCACACATT-ATGAACATCTGATG-TCTGATCGGGGTAC 586
QY 750 CAGCGTACGCTTCTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 809
DB 585 CAGCGTACGCTTCTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 526
QY 810 CCACGCGCTCCGATGATTCAGCGTGGCACCAGAAAGACATCATCCACGCTGA 869
DB 525 CCACGCGCTCCGATGATTCAGCGTGGCACCAGAAAGACATCATCCACGCTGA 466
QY 870 GGATGGAAAGGTACAGGTGACCCGCGCAGACCAAGCCCGATGAGATTAGCCAA 929
DB 465 GGATGGAAAGGTACAGGTGACCCGCGCAGACCAAGCCCGATGAGATTAGCCAA 406
QY 930 GACCGTGGCTGATCTGTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 989
DB 405 GACCGTGGCTGATCTGTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 346
QY 990 GGTGATGATGCTTCTTGGGAAGTGAACAAGCTCATTAAGACGCTGTTGCA 1049
DB 345 GGTGATGATGCTTCTTGGGAAGTGAACAAGCTCATTAAGACGCTGTTGCA 286
QY 1050 TATGCTCTGCTGTAACCTGTAACCCCATCATCTATGCTCTGAGAGTAAGA 1109
DB 285 TATGCTCTGCTGTAACCTGTAACCCCATCATCTATGCTCTGAGAGTAAGA 226
QY 1110 CTTGGGACACGCTTCCGAGAGATGTTCCCTCTTGTGAAGGACTGGCGACCTTGA 1169
DB 225 CTTGGGACACGCTTCCGAGAGATGTTCCCTCTTGTGAAGGACTGGCGACCTTGA 166
QY 1170 TAAACAGATGGGGGACTCGGACTGCTGCAAAACGGAACAATGACGCAAGTTCA 1229
DB 165 TAAACAGATGGGGGACTCGGACTGCTGCAAAACGGAACAATGACGCAAGTTCA 106
QY 1230 CAGGCGCGGAGAAAGCTGATCAAGACAGGTCAAGATTGCAAGTAACCATGCTGT 1289
DB 105 CAGGCGCGGAGAAAGCTGATCAAGACAGGTCAAGATTGCAAGTAACCATGCTGT 46
QY 1290 GTTCAAGACAGCTGCTGCGGAG 1311
DB 45 GTTCAAGACAGCTGCTGCGGAG 24
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RESULT 12

CC202312/c 1151 bp DNA linear GSS 09-MAY-2003
LOCUS
DEFINITION
CC261-70E11_Sp6.1 CH261 Gallus gallus genomic clone CH261-70E11,
genomic survey sequence.

CC202312
VERSION
CC202312.1 GI:30482109
KEYWORDS
GSS.
SOURCE
Gallus gallus (chicken)
ORGANISM

REFERENCE
1 (bases 1 to 1151)
Krentzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
Warren,W., Graves,T., Mardis,E. and Wilson,R.
Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

AUTHORS
Krentzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
Warren,W., Graves,T., Mardis,E. and Wilson,R.
TITLE
Gallus gallus BAC End Reads
JOURNAL
Unpublished (2003)
CONTACT: Richard K. Wilson
COMMENT
Genome Sequencing Center
Washington University School of Medicine
Email: submis@wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTAGTGACACTATAG
Class: BAC ends
High quality sequence start: 39
High quality sequence stop: 737.

FEATURES

source

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CH261 Female Chicken library - for library and clone  
ordering information: http://www.chori.org/bacpac"
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ORIGIN

Query Match 44.9%; Score 592.2; DB 12; Length 1151;
Best Local Similarity 79.3%; Pred. No. 2.9e-143;
Matches 727; Conservative 0; Mismatches 188; Indels 2; Gaps 2;

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QY 128 TGAATTAACAAGATTTTACAAAGTCTCTCTCTCTCAAGG-AGATAGGAGAAC 186
DB 949 TGAATTAACAAGATTTTACAAAGTCTCTCTCTCTCAAGG-AGATAGGAGAAC 890
QY 187 ATCCAGTGGGAGAACTTCATGACATAGAGTGTTCATGCTCTGAACCCAGCCAG 246
DB 889 ATCCAGTGGGAGAACTTCATGACATAGAGTGTTCATGCTCTGAACCCAGCCAG 830
QY 247 CAGCTGGCAATGACGCTGCTGCTCA-CGCTGGGCACTTCAAGGCTCGAAGACCT 305
DB 829 AAGTGGGCAATGACGCTGCTGCTCA-CGCTGGGCACTTCAAGGCTCGAAGACCT 770
QY 306 CTTGTGCTGTCGCTCATCTCTCACTCCGAGAGCTCCGCTGACAGGCTTCTCAACTT 365
DB 769 CTTGTGCTGTCGCTCATCTCTCACTCCGAGAGCTCCGCTGACAGGCTTCTCAACTT 710
QY 366 CATCGGACGCTGCGGCTGGGAGACCTCTCGGGAGTGTCAATTTTGTCAAGCTTCAT 425
DB 709 CATCGGACGCTGCGGCTGGGAGACCTCTCGGGAGTGTCAATTTTGTCAAGCTTCAT 650
QY 426 TGACTTCAAGCTTCCACCGGAAGATAGCGGACAGTGTTCGTTCAATCGGGTGG 485
DB 649 TGACTTCAAGCTTTCACCGGAAGATAGCGGACAGTGTTCGTTCAATCGGGTGG 590
QY 486 GGTCAAGGCTCTTCACTGCTCCGTTGGGAGAGCTGTTCTCAAGGCAATGACAGGTA 545
DB 589 AGTTACAGGCTCTTCAAGGCTCCGTTGGGAGAGCTGTTCTCAAGGCAATGACAGGTA 530
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QY	546	CATATTCATTCACAGGCCCCCTGGCCCTTTAAAGAGATTGTCAACAGGCCCAAGGCCGTGAT	605
Db	529	CATATCTATACAGAGGCCACTAGCTTACAAAGAATTGTAAACCCAGCAAGGCTGTCTGT	470
QY	606	AGCGTTTTCCTGATATGTGAGCCATPAGCCATTGTGATGCGCGTGTCTCTTGGGCTG	665
Db	469	TGCGTTTTTGTGTGATGTGAGCCATTCGCCATTGTAAATAGCTGTCTTCCGCTGTGCGCTG	410
QY	666	GAACCTGGAGAAATCTGCATCTGTATTGGCTGAGACATTTTCCACACATTGATGAAACCTA	725
Db	409	GAATCTGCAAAAAGCTCAACTCTGTGTGTTCAGACATATTTCCCTCTCATATGATGAGCGTA	350
QY	726	CTGATGTTCTGGAATCGGGGTACCAAGCGTACTGCTTCTGTTCAATCGTGAATGCGTACAT	785
Db	349	CTCATATGTTCTGGAGATGGGGGTACACAGAGGTCTCTTGTGTTCAATGTGCTATAT	290
QY	786	GTATATTCCTCGGAAGGCTCAACAGCAAGCCGTCGCAATGATTTAGAGGCTGGACCCAGAA	845
Db	289	GTAACATCTGTGGAAGGCGCAAGCCAGCTGTTGTGCAATGCTTCAACGCGCGCAAGCAGAA	230
QY	846	GAGCATCATCATCCACAGTCTGAGGATGGGAAGGTACAGGTGACCCGCGCAGAACCAAGC	905
Db	229	AAGCATATATCATTCAGAGTACGGAGGATGTTAAAGTACAGATCACTAAGACTGTATCAAA	170
QY	906	CCGATATGACATTAGTATGAGTAAAGCAAGACCTGTGCTCTGATCTCTGTGAGTGTGATCATCTG	965
Db	169	TCTGATGACATCAAGGTATGCAAAACCTTGCTCTTAATCTAGTCGTTTAAATCAATATG	110
QY	966	CTGGGGCCCTCTGCTTGCAATCATGATGTATGATGTCTTTGGGAAGATGAACAAGCTCAT	1025
Db	109	CTCGGGCCCTCTCTCGCCATTAATGTGTACGATGTCTTTGGGAAATGAACAAGCTCAT	50
QY	1026	TAAGACGGTGTTCAT	1042
Db	49	CAAGACTGTCTTCTCTT	33

RESULT	13
LOCUS	DN515498/c
DEFINITION	DN515498 680 bp mRNA linear EST 10-MAR-2005 1252753 MARC 7BOV Bos taurus cDNA 3' , mRNA sequence.
ACCESSION	DN515498
VERSION	DN515498.1 GI:60725688
KEYWORDS	EST.
SOURCE	Bos taurus (cattle)
ORGANISM	Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Peccora; Bovidae; Bovinae; Bos. 1 (bases 1 to 680) Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chtlco-Mckown,C.G., Wray,D.B. and Keefe,J.W.. A second set of bovine ESTs from pooled-tissue normalized libraries unpublished (2003) Contact: Smith TPJL USA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel.: 402 762 4366 Fax: 402 762 4390 Email: smitht@mail.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329. Plate: RLK8030 row: L column: 20 Seq primer: TAGAAAGCACTGTCAGG.	

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FEATURES
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ORIGIN

/note="vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI, Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embryos."

Query Match	43.8%;	Score 577.6;	DB 9;	Length 680;
Best Local Similarity	90.6%;	Pred. No. 1.6e-139;		
Matches	616;	Conservative	0;	Mismatches 64; Indels 0; Gaps 0;
QY	224	TCATGTCCTGGAACCCAGCCAGCAGAGCTGGCCCATTTGACGTCCTGTGCTCTTAACGCTGGGCA	283	
Db	680	TCATGATCTCGAACCACCCAGCAGAGAGCTGGCCCATTCGCTGTGCTTTCCCTCCATCGTTGGGCA	621	
QY	284	CCTTCAGGGTCCTGGGAACCTCCTGGTGGCTGGACGTCATCCCTCACTCCCGAGCCTCC	343	
Db	620	CCCTTCAGGGTCCTGGGAACCTGCTGGTGGCTGGACGTCATCCCTCACTCCCGAGCCTCC	561	
QY	344	GCTCAGAGCCTTCCTCAACACTTCACGCGAGCCTGGCGGTGGGAGACCTTCCTGGGGAGTG	403	
Db	560	GCTCGCGGCCCTCTTACCACTTATCCGAGCCTCGAGCTGCGCATCTCTCGTGGAGAGCG	501	
QY	404	TCATTTTGTCTACAGCTTCAATGACTTCCACGCTGTTCACCGCAAAATAGCCGCAAG	463	
Db	500	TCATCTTCGCTATAGCTTGTGTGACATTCCACGAGTGTCCACCCGAAAGACAGCCCCCAAG	441	
QY	464	TGTTTCTGTTCAAACTGGGTGGGGTCAAGGCTCTCTTCACTGCTCCGTGGGAGCCTGT	523	
Db	440	TGTTTCTGTTCAAACTGGGTGGGGTCAAGGCTCTCTTCACTGCTCCGTGGGAGCCTGT	381	
QY	524	TCCTCACAGCATCGACAGGTACATATCCATTCACAGGCCCTCTGACCTATTAAGAGATTG	583	
Db	380	TCTTCACGGCCATTCGACAGGTACATATCCATTCACAGGCCCTCTGACCTATTAAGAGATTG	321	
QY	584	TCACCAAGGCCCAAGGCCGTGGTAGCGTTTTCCTGATGTGAGCAATGACCATTTGTGATCG	643	
Db	320	TCACAGGCCCAAGGCCGTGGTAGCGTTTTCCTGATGTGAGCAATGACCATTTGTGATCG	261	
QY	644	CCGTGCTGCTCTCTTGGGCTGGAACCTGCGAAGAACTGCAATCTGTTTGGCTCAGACATTT	703	
Db	260	CCGTGCTGCTCTCTTGGGCTGGAACCTGCGAAGAACTGCAATCTGTTTGGCTCAGACATTT	201	
QY	704	TCCCAACATTTGATGAAGAACTCACTGATGTTTCGAGATCGGGGTCAACAGGCTACTGCTTC	763	
Db	200	TCCCTCTCATCGAAGAACTCACTGATGTTTCGAGATCGGGGTCAACAGGCTACTGCTTC	141	
QY	764	TGTTCACTGATGATGCTACATGATATTTCTCTGGAAGGCTCACAGCCAGCCGCTCCGCA	823	
Db	140	TGTTCACTGATGATGCTACATGATATTTCTCTGGAAGGCGCACAGCCAGCTGTCTCGCA	81	
QY	824	TGATTCAGCGTGGCAACCCAGAAAGCATCATTCACAAGTCTGAGAGATGGAAAGGTAC	883	
Db	80	TGATTCAGCGTGGTACCCAGAAAGCATCATTCACAAGTCTGAGAGATGGCAAGGTGC	21	
QY	884	AGGTGACCCGGCCAGACCA 903		
Db	20	AGGTGACAGGCTCCGAAAAA 1		

RESULT 14	
LOCUS	BUT0705501
DEFINITION	BUT0705501 780 bp mRNA linear EST 15-JUL-2003
ACCESSION	U1-M-FOO-cac-a-11-0-UI.r1 NIH BMAP_F00 Mus musculus cDNA clone
VERSION	IMAGE:6409234 5', mRNA sequence.
KEYWORDS	BUT0705501 BUT0705501.1 GI:23635044
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
	Sciuromorphi; Muridae; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 780)

with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., Program coordinator."

ORIGIN

Query Match	43.2%;	Score 570.8;	DB 4;	Length 789;
Best Local Similarity	87.3%;	Pred. No. 1e-137;		
Matches 647;	Conservative 0;	Mismatches 90;	Indels 4;	Gaps 2;
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DB	49	ACTTCCTTCAGGGGTAGTCCCTTCCAGAAAAGATGACGGCAGAGACAACTCCCGTTG	108	
QY	112	GTCCAGC---AGACCAAGGTGAACATTCAGAAATTTTACAAACAAGTCTCTCGTCTTC	168	
DB	109	GTTCAGCAGGAGACAAACCAACATTCAGAGTTCTATACAAAGTCTCTCTCATGCTTC	168	
QY	169	AAGGAAATGAGAGAAATCCAGTGTGGGAGAACTTCATGACATAGAGTTCATG	228	
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QY	229	GTCTGAACCCGACGACAGCTGGCATTCAGTCTGTCTCCCTCAAGCTGGGCACTTC	288	
DB	229	ATTCTGAATCCGACGACAGCTGGCATGCTGTCTGTCTCCCTCAAGCTGGGCACTTC	288	
QY	289	ACGGTCCTGGAACCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	348	
DB	289	ACGGTTCGGAACCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	348	
QY	349	AGGCTTCCTCAACATTCATCCGACGCTGGCGGTGGCAGACCTCTCGGGAGTGCATT	408	
DB	349	AGGCTTCCTCAACATTCATTCGAGCCCTGGCGGTGGCAGATCTCTCGGAAAGTGCATC	408	
QY	409	TTTGTCTACAGCTTCATGACTTTCACGCTGTTCACCGCAAGATAGCCGCAAGCTGTT	468	
DB	409	TTTGTCTACAGCTTCATGACTTTCACGCTGTTCACCGCAAGATAGTCCATGTGTTT	468	
QY	469	CTGTTCAACTGGGTGGGTGCAAGGCTCTTCATCTGCTCGGTGGGCAAGCTGTCTTC	528	
DB	469	CTGTTCAACTGGGTGGGTGTAACGCTCTTCATCAGCACTGTGGGCAAGCTGTCTTC	528	
QY	529	ACAGCCATGACAGGATCATATTCATTCACAGGCCCTGAGCTATTAAGAGATTGTCAAC	588	
DB	529	ACGGCCATGACAGGATCATATTCATTCACAGGCCCTGTGGCTATTAAGAGATGTCAAC	588	
QY	589	AGGCCCAAGGCGGTGTAGCGTTTGTCTGTATGTGACCAATAGCCATTGTATCGCCGTG	648	
DB	589	AGGCCCAAGGCGGTGTAGCGCTTTGTCTGTATGTGACCAATAGTAATGTCTGTG	648	
QY	649	CTGGCTCTCTGGGCTGGAACGCGGAAATGCAATCTGTTGCTCAGACATTTTCCCA	708	
DB	649	TTCCTCTCTCTGGCTGGAACGCGGAAATGCAATCTGTTGCTCAGACATCTTCCCA	708	
QY	709	C-ACATTTGATGAACCTTACCTGATGTTCTGATCGGGGTCAACGAGGTACTGCTCTGTT	767	
DB	709	CTCCATTTGATGANACCTTACTGATGTTCTGATCGGAGTCAACAGTGTGCTGTGCTTT	768	
QY	768	CATCGTATGCGTACATGTA	788	
DB	769	CATGTGTATGATACATGTA	789	

Search completed: June 17, 2006, 03:36:39
Job time : 6943 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2006, 23:32:16 ; Search time 287 Seconds

(without alignments)
8605.797 Million cell updates/sec

Title: US-10-521-428a-1

Perfect score: 1320
Sequence: 1 atgagtcgacccagatg.....cgtctgcgagcctctgta 1320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1256.2	95.2	2135	US-09-016-434-1450	Sequence 1450, Ap
2	1256.2	95.2	2135	US-09-023-655-1469	Sequence 1469, Ap
3	1254.6	95.0	1419	US-09-826-509-468	Sequence 468, App
4	245.2	18.6	1790	US-09-016-434-1359	Sequence 1359, Ap
5	245.2	18.6	1790	US-09-023-655-1398	Sequence 1398, Ap
6	240.4	18.2	1083	US-09-826-509-470	Sequence 470, App
7	96.8	7.3	2250	US-08-763-938-1	Sequence 1, Appli
8	92.4	7.0	1434	US-09-016-434-1310	Sequence 1310, Ap
9	92.4	7.0	1771	US-07-969-267B-1	Sequence 1, Appli
10	92.4	7.0	1771	US-09-168-510-1	Sequence 1, Appli
11	92.4	7.0	1771	US-10-277-078-1	Sequence 1, Appli
12	90.8	6.9	1434	US-09-826-509-492	Sequence 492, App
13	90.8	6.9	1673	US-07-791-926A-1	Sequence 1, Appli
14	90.8	6.9	1673	US-08-383-781B-1	Sequence 1, Appli
15	87	6.6	1535	US-09-964-956-14	Sequence 14, Appli
16	85.2	6.5	1621	US-08-722-001-13	Sequence 13, Appli
17	85.2	6.5	2002	US-09-016-434-1172	Sequence 1172, Ap
18	81.8	6.2	2308	US-07-686-591-3	Sequence 3, Appli
19	81.8	6.2	2308	US-07-970-715-3	Sequence 3, Appli
20	79.8	6.0	1776	US-08-722-001-29	Sequence 29, Appli
21	79.8	6.0	2140	US-08-334-698-1	Sequence 1, Appli
22	79.8	6.0	2140	US-08-228-932-1	Sequence 1, Appli
23	79.8	6.0	2140	US-08-468-939-1	Sequence 1, Appli

24	79.8	6.0	2140	US-08-406-855A-1	Sequence 1, Appli
25	79.8	6.0	2140	US-08-722-190-1	Sequence 1, Appli
26	79.8	6.0	2140	US-08-244-354-1	Sequence 1, Appli
27	79.8	6.0	2140	US-09-206-899-1	Sequence 1, Appli
28	79.8	6.0	2140	US-09-444-783-1	Sequence 1, Appli
29	79.8	6.0	2140	US-09-688-415-1	Sequence 1, Appli
30	79.8	6.0	2140	US-09-444-783-1	Sequence 1, Appli
31	79.8	6.0	2140	PCT-US95-04203-1	Sequence 1, Appli
32	78	5.9	1738	US-08-334-698-3	Sequence 1, Appli
33	78	5.9	1738	US-08-228-932-3	Sequence 3, Appli
34	78	5.9	1738	US-08-468-939-3	Sequence 3, Appli
35	78	5.9	1738	US-08-406-855A-3	Sequence 3, Appli
36	78	5.9	1738	US-08-722-190-3	Sequence 3, Appli
37	78	5.9	1738	US-08-244-354-3	Sequence 3, Appli
38	78	5.9	1738	US-09-206-899-3	Sequence 3, Appli
39	78	5.9	1738	US-09-444-783-3	Sequence 3, Appli
40	78	5.9	1738	US-09-688-415-3	Sequence 3, Appli
41	78	5.9	1738	US-09-016-434-1402	Sequence 1402, Ap
42	78	5.9	1738	US-09-444-783-3	Sequence 3, Appli
43	78	5.9	1738	PCT-US95-04203-3	Sequence 3, Appli
44	76.4	5.8	921	US-08-722-001-17	Sequence 17, Appli
45	76.4	5.8	1567	US-08-722-001-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1
US-09-016-434-1450
Sequence 1450, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sealhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: 09/016,434
APPLICATION NUMBER: 09/016,434
CLASSIFICATION: HERMITH
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
FAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1450:
SEQUENCE CHARACTERISTICS:
LENGTH: 2135 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9736236

Issued 12/31/02
7/30/98

US-09-016-434-1450

Query Match 95.2%; Score 1256.2; DB 3; Length 2135;
Best Local Similarity 99.4%; Pred. No. 8.3e-315;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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52 ACTGACCTCTGGGAGTCCCTTCCAGAGATGATGCGGGGAGACACCCCAAGCTA 111
Db ACTTCTTTAGGAGAGTCCCTTCCAGAGATGATGCGGGGAGACACCCCAAGCTA 301
Qy 112 GTCCAGCAGACCAAGTGAACATTACAGATTTTACAAAGTCTCTCTGCTTCAAG 171
Db GTCCAGCAGACCAAGTGAACATTACAGATTTTACAAAGTCTCTCTGCTTCAAG 361
Qy 172 GAGAAATGAGAGACATCCAGTGTGGGAGAACTTCATGACATGAGTGTTCATGTC 231
Db GAGAAATGAGAGACATCCAGTGTGGGAGAACTTCATGAGCATGAGTGTTCATGTC 421
Qy 232 CTGAACCCGACGACAGCTGGGACATGCAAGTCTGCTCCCTCAAGCTGGGACCTTCAAG 291
Db CTGAACCCGACGACAGCTGGGACATGCAAGTCTGCTCCCTCAAGCTGGGACCTTCAAG 481
Qy 292 GTCCGAGAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 351
Db GTCCGAGAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
Qy 352 CCTTCTTCACTTATGCGAGCTGCGGTGGAGACCTCTCTGGGAGTGTCAATTTT 411
Db CCTTCTTCACTTATGCGAGCTGCGGTGGAGACCTCTCTGGGAGTGTCAATTTT 601
Qy 412 GTCTACAGCTTCATGATCTTCCAGGTGTCCACGCAAGATAGCCGACGCTGTTCTG 471
Db GTCTACAGCTTCATGATCTTCCAGGTGTCCACGCAAGATAGCCGACGCTGTTCTG 661
Qy 602 GTCTACAGCTTCATGATCTTCCAGGTGTCCACGCAAGATAGCCGACGCTGTTCTG 661
Qy 472 TTCAAACTGGGTGGGTGCAAGCTCTTCACTGCTCTGCTGGGAGCTGTTCTGCA 531
Db TTCAAACTGGGTGGGTGCAAGCTCTTCACTGCTCTGCTGGGAGCTGTTCTGCA 721
Qy 532 GCCATCGACAGTATATATATATATATATATATATATATATATATATATATATAT 591
Db GCCATCGACAGTATATATATATATATATATATATATATATATATATATATAT 781
Qy 722 GCCATCGACAGTATATATATATATATATATATATATATATATATATATATAT 781
Qy 592 CCCAAGGCGGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
Db CCCAAGGCGGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 841
Qy 782 CCCAAGGCGGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 841
Qy 652 CCTCTCTGGGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 711
Db CCTCTCTGGGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
Qy 712 ATGATGAACTTACTGATGCTTCTGAGATCGGGGTGCAAGGATCTGCTGCTGCTG 771
Db ATGATGAACTTACTGATGCTTCTGAGATCGGGGTGCAAGGATCTGCTGCTGCTG 961
Qy 902 ATGATGAACTTACTGATGCTTCTGAGATCGGGGTGCAAGGATCTGCTGCTGCTG 961
Qy 772 GTGATGCGTATATATATATATATATATATATATATATATATATATATATATAT 831
Db GTGATGCGTATATATATATATATATATATATATATATATATATATATATATAT 1021
Qy 962 GTGATGCGTATATATATATATATATATATATATATATATATATATATATATAT 1021
Qy 832 CGTGACCCAGAGAGATCATCATCAACGCTGAGATGAGATGAGATGAGATGAGAT 891
Db CGTGACCCAGAGAGATCATCATCAACGCTGAGATGAGATGAGATGAGATGAGAT 1081
Qy 1022 CGTGACCCAGAGAGATCATCATCAACGCTGAGATGAGATGAGATGAGATGAGAT 1081
Qy 892 CGGCGAGACCAAGCCGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 951
Db CGGCGAGACCAAGCCGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1141
Qy 1082 GTGATGATCATGCTGCGGCGCTCTGCTGCAATCATGATGATGATGATGATGATG 1011
Db GTGATGATCATGCTGCGGCGCTCTGCTGCAATCATGATGATGATGATGATGATG 1201
Qy 1142 GTGATGATCATGCTGCGGCGCTCTGCTGCAATCATGATGATGATGATGATGATG 1201
Qy 1012 ATGAACAAGCTCATTAAGAGCGGTGTTTGATTTCTGCAATGATGCTGCTGCTGCA 1071
Db ATGAACAAGCTCATTAAGAGCGGTGTTTGATTTCTGCAATGATGATGCTGCTGCTG 1261
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Qy 1072 ACCGTGAACCCCATCATCTATGCTCTGAGAGTAAAGACCTGGGACACGCTTTCCGGAGC 1131
Db ACCGTGAACCCCATCATCTATGCTCTGAGAGTAAAGACCTGGGACACGCTTTCCGGAGC 1321
Qy 1132 ATGTTTCCCTCTTGTGAAGGCACTGCGAGCTCTGTGATTAACAGATGAGGAGACTCGGAC 1191
Db ATGTTTCCCTCTTGTGAAGGCACTGCGAGCTCTGTGATTAACAGATGAGGAGACTCGGAC 1381
Qy 1192 TGCTGCAAAACACGCAACATGACAGCTGTTGACAGGGCCGCAAGAACTGCAATC 1251
Db TGCTGCAAAACACGCAACATGACAGCTGTTGACAGGGCCGCAAGAACTGCAATC 1441
Qy 1252 AAGGACAGGTCAAGATTGGCCAGATTAACATGCTGATGTCACAGACACGCTCGCGAG 1311
Db AAGGACAGGTCAAGATTGGCCAGATTAACATGCTGATGTCACAGACACGCTCGCGAG 1501
Qy 1312 GCTCTGTGA 1320
Db GCTCTGTGA 1510
```

RESULT 2

US-09-023-655-1469

; Sequence 1469, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESS: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023.655

; FILING DATE: HEREMITH

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1469:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2135 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK

; CLONE: 9736236

US-09-023-655-1469

Query Match 95.2%; Score 1256.2; DB 3; Length 2135;
Best Local Similarity 99.4%; Pred. No. 8.3e-315;

Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	52	ACTGACCTCTCTGGGAAGTCCCTTCCAAAGAAAGATGACTCGGGGAGCAACCCCGACGTA	111
Db	242	ACTTCCTTTAGGGGAAGTCCCTTCCAAAGAAAGATGACTCGGGGAGCAACCCCGACGTA	301
QY	112	GTCCGACGACACGAGTGAACTTACAGATTTTACAAAGAGCTCTCTGCTCTTCAAG	171
Db	302	GTCCGACGACACGAGTGAACTTACAGATTTTACAAAGAGCTCTCTGCTCTTCAAG	361
QY	172	GAGAAATGAGGAACAATCCAGTGTGGGGGAACCTTCAATGACATAAAGTTCATAGTGC	231
Db	362	GAGAAATGAGGAACAATCCAGTGTGGGGGAACCTTCAATGACATAAAGTTCATAGTGC	421
QY	232	CTGAACCCGACGACGCTGCGCAATGAGTCTGTCCCTCAAGCTGCGGACCTTCAAG	291
Db	422	CTGAACCCGACGACGCTGCGCAATGAGTCTGTCCCTCAAGCTGCGGACCTTCAAG	481
QY	292	GTCCCTGAGAAACTCTGTGTGTGTGCGTCATCTTCACTCCGACAGCTCCGCTGACG	351
Db	482	GTCCCTGAGAAACTCTGTGTGTGTGCGTCATCTTCACTCCGACAGCTCCGCTGACG	541
QY	352	CCCTTCTACCACTTACGCGGACGCTGCGGAGTGAGACCTCTCGGGGAGTGATTTT	411
Db	542	CCCTTCTACCACTTACGCGGACGCTGCGGAGTGAGACCTCTCGGGGAGTGATTTT	601
QY	412	GTCTACAGCTTCATTGACTTCCACGCTGTTCCACCGAAAGATAGCCGCAAGTGTTCG	471
Db	602	GTCTACAGCTTCATTGACTTCCACGCTGTTCCACCGAAAGATAGCCGCAAGTGTTCG	661
QY	472	TTCAAACTGGGGGGGTCAACGGCCCTTCCATCTGCTCCGTGGGACGCTGTTCTCA	531
Db	662	TTCAAACTGGGGGGGTCAACGGCCCTTCCATCTGCTCCGTGGGACGCTGTTCTCA	721
QY	532	GCCATCGACAGGTATATATCCATTACAGGCGCCCTGACCTATAGAGATTGTCAACG	591
Db	722	GCCATCGACAGGTATATATCCATTACAGGCGCCCTGACCTATAGAGATTGTCAACG	781
QY	592	CCCAAGGCGGTGTGATGCGTTTGTCTGATGTGACCATAGCCATTGTGATGCGCGTGTG	651
Db	782	CCCAAGGCGGTGTGATGCGTTTGTCTGATGTGACCATAGCCATTGTGATGCGCGTGTG	841
QY	652	CCTCTCCCGGGCTGGAACTGGGAGAACTGCAATCTGTTGTCCAGACATTTTCCACAC	711
Db	842	CCTCTCCCGGGCTGGAACTGGGAGAACTGCAATCTGTTGTCCAGACATTTTCCACAC	901
QY	712	ATTGATGAAACTTACTGATGTTCTGGAATCGGGGTCAACAGCGTACTGCTCTGATC	771
Db	902	ATTGATGAAACTTACTGATGTTCTGGAATCGGGGTCAACAGCGTACTGCTCTGATC	961
QY	772	GTGATAGGTATATGTATATTCTCTGAAAGGCTCAACGCAACGCGGTCCGATGATTCAG	831
Db	962	GTGATAGGTATATGTATATTCTCTGAAAGGCTCAACGCAACGCGGTCCGATGATTCAG	1021
QY	832	CGTGGCAACCAAGAGAGCATCATATCAACAGCTGAGGAATGGGAAGGTACAGGTAC	891
Db	1022	CGTGGCAACCAAGAGAGCATCATATCAACAGCTGAGGAATGGGAAGGTACAGGTAC	1081
QY	892	CGGCGACACCAAGCCCGCATGACATTAGTTAGCCCAAGACCTGTGCTCTGATCTGTGTG	951
Db	1082	CGGCGACACCAAGCCCGCATGACATTAGTTAGCCCAAGACCTGTGCTCTGATCTGTGTG	1141
QY	952	GTGTGTGATCATCTGTGTGGGCGCTCTGTGTAACATGAGGTATAGATCTTTTGGGAAG	1011
Db	1142	GTGTGTGATCATCTGTGTGGGCGCTCTGTGTAACATGAGGTATAGATCTTTTGGGAAG	1201
QY	1012	ATGAACAAGCTCATTTAAGACGGTGTTCATTTCTGACAGTATGCTCTGCTGCTGAACCTC	1071
Db	1202	ATGAACAAGCTCATTTAAGACGGTGTTCATTTCTGACAGTATGCTCTGCTGCTGAACCTC	1261
QY	1072	ACCGTGAACCCCATCATCTATATGCTCTGAGAGATTAAGACCTGCGACACGCTTCCGAGC	1131
Db	1262	ACCGTGAACCCCATCATCTATATGCTCTGAGAGATTAAGACCTGCGACACGCTTCCGAGC	1321

QY	1132	ATGTTCCCTCTTGGAAAGGCACTGGCAGACCCCTGGATTAACAGCAATGGGGGACTCGGAC	1191
Db	1332	ATGTTTCCCTCTTGGAAAGGCACTGGCAGACCTCTGGATTAACAGCAATGGGGGACTCGGAC	1381
QY	1192	TGCTCTGACAAACAGCAAAACATGACGACGAGTTTCACAGGAGCCGACAGAACTGCATC	1251
Db	1382	TGCTCTGACAAACAGCAAAACATGACGACGAGTTTCACAGGAGCCGACAGAACTGCATC	1441
QY	1252	AAGAGCACGGTCAAGATTGCCAAGGTAAACATGCTGTGTCCACAAGACACGTCTGCCGAG	1311
Db	1442	AAGAGCACAGTCAAGATTGCCAAGGTAAACATGCTGTGTCCACAAGACACGTCTGCCGAG	1501
QY	1312	GCTCTGTGA	1320
Db	1502	GCTCTGTGA	1510

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RESULT 3
US-09-826-509-468
: Sequence 468: Application US/09826509
: Patent No. 6806054
: GENERAL INFORMATION:
: APPLICANT: Lehmann-Bruinsma, Karin
: APPLICANT: Liaw, Chen W.
: APPLICANT: Lin, I-Lin
: TITLE OF INVENTION: NO. 6806054-Endogenous, Constitutively Activated Known G
: TITLE OF INVENTION: Protein-Coupled Receptors
: FILE REFERENCE: AREN-207
: CURRENT APPLICATION NUMBER: US/09/826,509
: CURRENT FILING DATE: 2001-04-05
: PRIOR APPLICATION NUMBER: 60/195,747
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: 09/170,496
: PRIOR FILING DATE: 1998-10-13
: NUMBER OF SEQ ID NOS: 589
: SOFTWARE: PatentIn Version 2.1
: SEQ ID NO 468
: LENGTH: 1419
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-826-509-468

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Query Match	95.0%	Score 1254.6	DB 3	Length 1419
Best Local Similarity	99.3%	Prod. No. 1.7e-314		
Matches 1260	Conservative	0	Mismatches 9	Indels 0
			Gaps	0
QY	52	ACTGACCTCCCTGGGAAAGTCCCTTCCAAAGAAAGATGACTGCGGGAGACAACCCCGACTA	111	
Db	151	ACTTCCTTTAGGGGAAAGTCCCTTCCAAAGAAAGATGACTGCGGGAGACAACCCCGACTA	210	
QY	112	GTCCAGACAGCAGGTGACATTACAGAAATTTTCAACAAGCTCTCTCGTCTTCAAG	171	
Db	211	GTCCAGACAGCAGGTGACATTACAGAAATTTTCAACAAGCTCTCTCGTCTTCAAG	270	
QY	172	GAGAAATGAGGAACATTCAGTGTGGGGAGAACTTCATGACATAGAGTTCATGATC	231	
Db	271	GAGAAATGAGGAACATTCAGTGTGGGGAGAACTTCATGACATAGAGTTCATGATC	330	
QY	232	CTGAAACCCCAAGCCAGCACTGGCCATTGCACTGCTGCTCTCAAGCTGGGACCTTCACG	291	
Db	331	CTGAAACCCCAAGCCAGCACTGGCCATTGCACTGCTGCTCTCAAGCTGGGACCTTCACG	390	
QY	292	GTCTTGAGGAACCTCGGTGCTGTGGGTCAATCCCACTCCCGAGACTCCGCTGCAGG	351	
Db	391	GTCTTGAGGAACCTCGGTGCTGTGGGTCAATCCCACTCCCGAGACTCCGCTGCAGG	450	
QY	352	CCTTCCTACCACTTCATGCGAGGCTGGCGGTGGCGAGACTTCCTGGGGAGTGTCAATTTT	411	
Db	451	CCTTCCTACCACTTCATGCGAGGCTGGCGGTGGCGAGACTTCCTGGGGAGTGTCAATTTT	510	
QY	412	GCTTACAGCTTCATGACTTCCAGTGTTCACCGCAAAAGATAGCCGCAACGTGTTCTG	471	

Db	511	GTCTACAGCTTCATTGAACCTTCCACAGTGTCTTCACCGCAAAAGATAGCCGAAGTGTTCGTG	570
Qy	472	TTCAAACTGGGTGGGGTCAAGGACCTCTTTCACCTGCTCCGTGGGCAAGCTGTTCCTCA	531
Db	571	TTCAAACTGGGTGGGGTCAAGGACCTCTTTCACCTGCTCCGTGGGCAAGCTGTTCCTCA	630
Qy	532	GGCAATCGACAGGTACATATCCATTCACAGGGCCCTGGGCTCTATTAAGAGATTTGTACCAAG	591
Db	631	GGCAATCGACAGGTACATATCCATTCACAGGGCCCTGGGCTCTATTAAGAGATTTGTACCAAG	690
Qy	592	CCCAAGGCGGTGGTGGCGTTTTCCTGTATGTGACCAATAGCAATGTATGCGCGTGTG	651
Db	691	CCCAAGGCGGTGGTGGCGTTTTCCTGTATGTGACCAATAGCAATGTATGCGCGTGTG	750
Qy	652	CCTCTCCTGGGCTGGAACTGCGAGAACTGCATCTGTTTGTCTCAGACATTTTCCACAC	711
Db	751	CCTCTCCTGGGCTGGAACTGCGAGAACTGCATCTGTTTGTCTCAGACATTTTCCACAC	810
Qy	712	ATTGATGAAACCTACCTGATGTTCCTGGAATCGGGGTACACAGGTATCTGCTTCTGTATC	771
Db	811	ATTGATGAAACCTACCTGATGTTCCTGGAATCGGGGTACACAGGTATCTGCTTCTGTATC	870
Qy	772	GTGATGTGGTACATGTATATTTCTCGGAAGGCTCACACAGCCGCTCGAGATTTAG	831
Db	871	GTGATGTGGTACATGTATATTTCTCGGAAGGCTCACACAGCCGCTCGAGATTTAG	930
Qy	832	CGTGGCACCCAGAAAGAGCATCATCACTCACAGTCTGAGATGGGAAGTACAGGTGACC	891
Db	931	CGTGGCACCCAGAAAGAGCATCATCACTCACAGTCTGAGATGGGAAGTACAGGTGACC	990
Qy	892	CGGCGAAGCCAAAGCCCGCATGGACATTAGGTTAGCCAAAGCCCTGTCTGTATCCTGGTG	951
Db	991	CGGCGAAGCCAAAGCCCGCATGGACATTAGGTTAGGAAGACCCGTGTCTGTATCCTGGTG	1050
Qy	952	GTGTTGATCATCTGTGCGGGCCCTGTGCTGCAATCATGGTATGATGTCTTTGGGAAG	1011
Db	1051	GTGTTGATCATCTGTGCGGGCCCTGTGCTGCAATCATGGTATGATGTCTTTGGGAAG	1110
Qy	1012	ATGAACAAGCTCATTAAGAAGGTGTTTGCATTTCTGACAGTATGCTCTGCTGTGAACCTCC	1071
Db	1111	ATGAACAAGCTCATTAAGAAGGTGTTTGCATTTCTGACAGTATGCTCTGCTGTGAACCTCC	1170
Qy	1072	ACCGTGAACCCCATCATCTATATGCTCTGAGAGTAAGAACCTGCGACACGCTTTCGGAGC	1131
Db	1171	ACCGTGAACCCCATCATCTATATGCTCTGAGAGTAAGAACCTGCGACACGCTTTCGGAGC	1230
Qy	1132	ATGTTTCCCTCTGTGGAAGGCACTGCGGAGCCTCTGAGTAAACAGATATGGGGGACCTCGAGC	1191
Db	1231	ATGTTTCCCTCTGTGGAAGGCACTGCGGAGCCTCTGAGTAAACAGATATGGGGGACCTCGAGC	1290
Qy	1192	TGCTGTGCAAAACGCAAAACATGACAGCAGGTGTTTCACAGGGCCGCAAGAAAGCTGCATC	1251
Db	1291	TGCTGTGCAAAACGCAAAACATGACAGCAGGTGTTTCACAGGGCCGCAAGAAAGCTGCATC	1350
Qy	1351	AAGAGCAAGGTCAAGATTTGCCAAGGTAACCATGTCTGTGTCCACAGACACGCTTCGAG	1410
Db	1411	GCTCTGTGA 1419	

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RESULT 4
US-09-016-434-1359
; Sequence 1359, Application US/09016434
; Patent No. 6500938
;
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1359:
SEQUENCE CHARACTERISTICS:
LENGTH: 1790 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g9407806
US-09-016-434-1359

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[illegible]

647 TGCTGCTCTCCTGGGCTGGAACTGGAGAACTGCATCTGTTTGTCTGACATTTTCC 706
623 ACTTGCCCCCTCAGGAGTGAAGTCTGTGCCAGGC-----CTGTCTGACCTTTTCC 676
707 CACACATTGATGAACCTACCTGATGTTCTGATTCGAGGCTCACCAGCGTACTCTCTG 766
677 CACTGATCCCAATGACTACCTGCTAGCTGCTCTCTGTTGATGCTTCTCTTTCCG 736
767 TCATCTGTATGCTACATGATATATTCTCTGAAAGGCTCACAGCCAGCCGCTCCGATGA 826
737 GAATCATCTACACCTATGGGCGATGTTCTCTGAAAGGCCCATCAGCATGTCGACGCTT-- 794
827 TTCAGGCTGGACCCAGAAAGACATCATTCACACGCTTGGAGATGGGAAGTACAG 886
795 -----GTCCTGGCCACAGAGACAGGCAAG 817
887 TGACCCGGCCAGACCAAGCCCGCATGAGCATTAAGTTAGCAAGACCTGTCTGATCC 946
818 TGCCAGGAATGGCCCGAATGAGGCTGATGTAGAGTTGGCCAGACCTTAGAGGCTTAGT 877
947 TGGTGTGTTGATCATCTGCTGGGACCTCTGCTTGCAATCATGTGTATGATGCTTTG 1006
878 TGGCTGTGCTCTCATCTGTTGGTTCCAGTGTGCTGCCCTCANTGCCCCAGCCTGGCA 937
1007 GGAAGATGAACAAGCTCATTAAGACGCTGTTTGCATTCTGCAATAGCTCTGCTGCTGA 1066
938 CTACGCTCAGTGAACCAAGGTCAGAAAGGCTTGTCTTCTGCTCCAGCTGTGCTCATCA 997
1067 ACTCCAGCTGAACCCCATCATCTATGCTCTGAGAGTAAAGACCTGGACACGCTTTCC 1126
998 ACTCATGATCAACCTGTCTGATCTATGCTCTTACGAGAGTGAAGATCCGCTCTGCCCC 1057

RESULT 5
US-09-023-655-1398; Sequence 1398, Application US/09023655
; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cooke, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1398:

; INFORMATION FOR SEQ ID NO: 1398:

SEQUENCE CHARACTERISTICS:
; LENGTH: 1790 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9407806
US-09-023-655-1398

Query Match 18.6%; Score 245.2; DB 3; Length 1790;
Best Local Similarity 55.9%; Pred. No. 2.3e-53;
Matches 537; Conservative 0; Mismatches 378; Indels 45; Gaps 2;

167 TCAAGAGAAATGAGAGAAATTCAGATGTCGAGAGAACTTCAATGACATGATGTTTCA 226
143 TGACAGAGATGACCAATGAGCTCCAGAGATGGCTTGGATTCCAACTTATGAAGATTACA 202
227 TGGTCTTGAACCCAGCCAGAGCTGGCCATTGCACTGTCTGTCTTCCACGCTGGCACTT 286
203 TGATCTGTAGTGTCCCAAGAAACAGCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGT 262
287 TCACGCTCTGAGAGAACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 346
263 TAAATGCTTGGAGAACTGT 322
347 GCAGGCTTCTTACCACTTCATTCGAGCTGGCGAGTGGCAGACCTCTGAGAGTGTCA 406
322 GGAAGCTTCATACCTGTTTCAATTTGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 382
407 TTTTGTCTACAGCTTTCATTTGACTTTCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 466
383 TCTTTGATGACGCTTGT 442
467 TTTCTGTCAAATGAGGATGGGATCACGAGCTCTCTCACTGCTCCGAGGAGCTGTGTTC 526
443 TCTCTGTGAAGATTGGCAGCTGATCTATGACCTTTCACAGCTCTGTGTGTGTGTGTGTGT 502
527 TCACAGCCATGACAGATCATATATCATTCACAGGCCCCCTGTGCTATTAAGAGATTGTCA 586
503 TCACCGCATTTGACCGATATACCTCTGCGCGTATTCACACCTTCTCAAAAGCTGTGTCA 562
587 CCAGGCCAAGGCGCTGT 646
563 CCGGTGAAGGCACTGT 622
647 TGCTGCTCTCTCTGGGCTGGAACCTGCGAAGAACTGATCTGTGTGTGTGTGTGTGTGTGT 706
623 ACTTGCCCCCTCAGGAGTGAAGTCTGTGCCAGGC-----CTGTCTGACCTTTTCC 676
707 CACACATTGATGAACCTACCTGATGTTCTGATCGAGGCTCAACGCTACTGCTTGT 766
677 CACTGATCCCAATGACTACCTGCTGAGCTGTGCTCTCTGTATATGCTTCTTTTCCG 736
767 TCATCTGTATGCTGATCATGATATATTCTCTGAAAGGCTCACAGCCAGCCGCTCCGATGA 826
737 GAATCATCTACACCTATGAGGATGTTCTCTGAAAGGCCCATCAGATGTGTGCACTT-- 794
827 TTCAGCTGGACCCAGAAAGACATCATTCACACGCTTGGAGATGGGAAGTACAG 886
795 -----GTCCTGGCCACAGAGACAGGCAAG 817
887 TGACCCGGCCAGACCAAGCCCGCATGACATTAAGTTAGCCAAAGACCTGTCTGATCC 946
818 TGCCAGGAATGGCCCGAATGAGGCTGATGTAGAGTTGGCCAAAGACCTTAGAGGCTTAGT 877
947 TGGTGTGTTGATCATCTGCTGGGACCTCTGCTTGCAATCATGTGTATGATGCTTTG 1006
878 TGGCTGTCTCTCATATCTGT 937
1007 GGAAGATGAACAAGCTCATTAAGACGCTGTTGCTTGTGAGTATGCTGCTGCTGCTGA 1066
938 CTACGCTCAGTGAACAGGTCAAGAGGCTTTGCTTCTGCTCCATGCTGTGCTCATCA 997

QY	1067	ACTCCACCGTGAACCCCATCATATGCTGTGAGGATGAAGACCTGGACACAGCTTTCC	1126
Db	998	ACTTCATGGTCAACCTCTGCATCTATGCTTACGAGAGTGAAGATCCGCTCTCTGCC	1057

RESULT 6

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US-09-826-509-470
? Sequence 470, Application US/09826509
? Patent No. 6806054
? GENERAL INFORMATION:
? APPLICANT: Lehmann-Brulnema, Karin
? APPLICANT: Liaw, Chen W.
? APPLICANT: Lin, I-Lin
? TITLE OF INVENTION: NO. 6806054- Endogenous, Constitutively Activated Known G
? TITLE OF INVENTION: Protein-Coupled Receptors
? FILE REFERENCE: AREN-207
? CURRENT APPLICATION NUMBER: US/09/826,509
? CURRENT FILING DATE: 2001-04-05
? PRIOR APPLICATION NUMBER: 60/195,747
? PRIOR FILING DATE: 2000-04-07
? PRIOR APPLICATION NUMBER: 09/170,496
? PRIOR FILING DATE: 1998-10-13
? NUMBER OF SEQ ID NOS: 589
? SOFTWARE: PatentIn Version 2.1
? SEQ ID NO 470
? LENGTH: 1083
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-826-509-470

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Query Match	18.2%;	Score 240.4;	DB 3;	Length 1083;
Best Local Similarity	55.6%;	Pred. No. 3.3e-52;		
Matches 534;	Conservative 0;	Mismatches 381;	Indels 45;	Gaps 2;

Oy	167	TC AAGGA AATG AAGGA AACA TC CAGTGTGGGGA AACTTCA TGA GCA TTA GAGTGTTC CA	226
Db	17	TG ACGAG ATAG CCAATGG CTTC CAA GAGATGG CTTG GATTCC AACCTTATGA AGATTACA	76
Oy	227	TG GTCTGA A C C C C C C A G C C A G C A G C T G G C C A T T G C A G T C C T G C C T C A C G C T G G G A C C T	286
Db	77	TG ATCTGA TGGTGTCC CAGA AAGACG CTGTTC GTGTGTGG CACTCTTCTGGG CCTGC	136
Oy	287	TC A G G T C T T G G A G A A C C T C C T G G T G C T G T G C A T C T C A C T C C C G A G C C T G C G C T	346
Db	137	T A A G T C C C T G A G A A C G T G C T G C T C T A T C T A T C C T G T C C T C C A C C A A C T C C G C C	196
Oy	347	G C A G G C C T T C C T A C C A C T T C A T C G G C A G C C T G G C G G T G G A G A C C T C C T G G G G A G T G C A	406
Db	197	G G A G C C C T A C C T G T T C A T T G G C A G C T T G G C T G G G G C T G A C T T C C T G G C A G T G T G G	256
Oy	407	T T T T T G T C T A C A G C T T C A T T G A C T T C C A C G T G T T C A C C G A A A G A T A G C G C A A C G T G	466
Db	257	T C T T T T G A G A G C T T T G T G A A T T C A A T G T T T C A A G T G T G A T T C C A A G C T G C T C T	316
Oy	467	T T C T G T T C A A A C T G G G T G G G G C A C G G C C T C C T C A C T G C C T C G G T G G G A C G C C T G T T C C	526
Db	317	T C T G C T A A A G T T G G C A G C G T G A C T A T G A C C T T C A G C C T C T G T G G G T A G C C T C C T G C	376
Oy	527	T C A G A C A T G A C A G G T A C A T A T C A T T C A G A G C C C C T G G C C T A T A A G A G A T T G T C A	586
Db	377	T G A C C G C A T T G A C G A T A C C T C T G C G C G T A T C A C A C T T C C T A C A A A G C T G C T C A	436
Oy	587	C C A G G C C C A A G C C G T G A G G T T T G A C T G A T G T G A C C A T A G C A T A G C A T T G A A T C G C G C	646
Db	437	C C C G T G A A G G C A C T G T G A C C C T G G G A T A T A T G G T G C C T C T C A G A C A C T A G C T T C C T	496
Oy	647	T G T G C C T C T C C T G G G C T G A A C T G C G A A A C T G A A C T G T T G C T C A G A C A T T T T C C	706
Db	497	A C T G C C C C C T A T G G A T G G A C T T G C T G C C C A G G C ----- C T G C T C T G A G C T T T T C C	550
Oy	707	C A C A C T T G A T G A A C C T A C C T G A T G T T C T G G A T G G G G T C A C A G C G T A C C T T C T T G T	766

Db	551	CACGATGCCCAATGACTACCTGCTGAGCGTGGCTCCGTTTCATGCGCTTCCTTTTCCG	61.0
QY	767	TCATCGTGATGCGTACATGATATTTCTTCGAAAGGCTCAGCGCCGTCGCATGTA	826
Db	611	GAATCATCTACACCTTAAGGCGATGTTCTTCGGAAGGCCCATCAGCATGTGGCAGCTT--	668
QY	827	TTTACGCGTGGACCCCAAGAAGCATATCATCCAAGTCGTGAGGATGGGAAGGTACAG	886
Db	669	-----GTCTGGCCACAGACAGCGAGG	691
QY	887	TGACCCCGCCAGACCAAGCCGCGCATGAGCATTTAGCTTAGCCAGACCTGTCCTGATCC	946
Db	692	TGCCAGAAATGCGCCGAAATGAGGCTGAAATGTGAGGTTGAAGAAACCTCTAGGGTAAATGT	751
QY	947	TGTGAGTGTGATCATCTGCTGGGGCCCTCTGCTTGCAATCANGTGTATGATGTCCTTGG	1006
Db	752	TGGCTGTGCTCTCATCTGTGTGGTTGCCAAGTGCTGGCCCTCATGCGCCACAGCCTGGCA	811
QY	1007	GGAAAGATGAACAGCTCATTTAAGCGGTGTTTGATTTCTGCAATGATGCTCTGCTGCTGA	1066
Db	812	CTAGCGCTCAGTGCACCAAGTCAAGAAAGGCGTTTGTCTCTCTCCATGCTGTGCTCTATCA	871
QY	1067	ACTCCACCGTGAACCCCATATCTAATGCTCGAGAGTAAGAACCTGCGACAGGCTTTC	1126
Db	872	ACTCATAGTCAACCCCTGTCACTCATCTCTCTACGAGTGAAGATCCGCTCCTCTGCCCC	931

RESULT 7

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US-08-763-938-1
; Sequence 1, Application US/08763938
; Patent No. 6140060
;
GENERAL INFORMATION:
;
APPLICANT: CHUN, Jerold J.M.
;
APPLICANT: HECHT, Jonathan H.
;
TITLE OF INVENTION: CLONED LYSPHOSPHATIDIC ACID
;
TITLE OF INVENTION: RECEPTORS
;
NUMBER OF SEQUENCES: 6
;
CORRESPONDENCE ADDRESS:
;
ADDRESS: Mikado, Marmelstein, Murray and Oram LLP
;
STREET: 665 15th Street, N.W., Suite 330 - G St. Lobby
;
CITY: Washington
;
STATE: DC
;
COUNTRY: USA
;
ZIP: 20005-5701
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Floppy disk
;
COMPUTER: IBM PC compatible
;
OPERATING SYSTEM: PC-DOS/MS-DOS
;
SOFTWARE: Patentin Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/08/763,938
;
FILING DATE: 12-DEC-1996
;
CLASSIFICATION: 800
;
ATTORNEY/AGENT INFORMATION:
;
NAME: JAHNS, Kristina M.
;
REGISTRATION NUMBER: 41,092
;
REFERENCE/DOCKET NUMBER: P8074-6018
;
TELECOMMUNICATION INFORMATION:
;
TELEPHONE: (202) 638-5000
;
TELEFAX: (202) 638-4810
;
INFORMATION FOR SEQ ID NO: 1:
;
SEQUENCE CHARACTERISTICS:
;
LENGTH: 2250 base pairs
;
TYPE: nucleic acid
;
STRANDEDNESS: single
;
TOPOLOGY: linear
;
MOLECULE TYPE: CDNA
;
US-08-763-938-1

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Query Match	7.3%	Score 96.8;	DB 3;	Length 2250;
Best Local Similarity	50.5%;	Pred. No. 5.9e-15;		
Matches 289;	Conservative 0;	Mismatches 277;	Indels 6;	Gaps 2;

FILING DATE: 05-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/551,448
FILING DATE: 10-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 140..1573
US-07-969-267B-1

Query Match 7.0%; Score 92.4; DB 2; Length 1771;

Best Local Similarity 51.4%; Pred. No. 7.4e-14;
Matches 213; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 247 CAGTGGCATTGACAGTCTGCTCCCTCAAGCTGGGACCTTCACGGTCTGGAGAACCTC 306
DB 257 CAGGTGTCACCGCTGCTGCTGTAACCTCATCATCTGAGACCTGCTGGGCAACGTG 316
QY 307 CTGTGCTGTGCTGCTCATCTCCGACGCTCCGCTGAGGCTTCTTCAACATTC 366
DB 317 CTGTGCTGTGCTGCTCATCTCCGACGCTCCGCTGAGGCTTCTTCAACATTC 376
QY 367 ATCCGACCTGGGCGGTGGAGACCTCCGCGGAGTGTCTTGTCTACAGCTTCATT 426
DB 377 ATCGTCTCTGGCCGTGTCAAGACCTTTTCGTGGCGCTGCTGTATGCTCCGGAAGCA 436
QY 427 GACTTCACAGTGTTCACCGCAAGATAGCCGCAAGTGTTCCTGTTCAAACTGGGTGG 486
DB 437 GTCCGCGAGGTGGCGGTACTGAGCCCTTTGAGAGGTCTGAGAGTCTGGGTGCTTC 496
QY 487 GTACAGGCTCTCTTCACTGCTCTCGTGGGACGCTGTTCTTCAAGCAATGACGTTAC 546
DB 497 GACATCATGTGCTCTCACTGCTCTCAATCTGAACTGTGTGCTCATGAGGTGACGCTAC 556
QY 547 ATATCATTTCAAGGCGCCCTGCGCTATAAGAGATTGTCAACAGGCGCAAGCGGTGTA 606
DB 557 TGGGCTATCTCAAGGCGCTTCCGCTACAGGCGCAAGATGATCAAGGCGACCTTGGTC 616
QY 607 GCGTTTTCCTGATGTGACCATAGCATTTGATGCGCGTCTGCTCTCTG 660
DB 617 ATGTGCGGCTGTGAGGACCTTGTCTCATCTCTTCACTCCGCTCAG 670

RESULT 10
US-09-168-510-1
Sequence 1, Application US/09168510
Patent No. 6468767
GENERAL INFORMATION:
APPLICANT: Weinsbank, Richard L.
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA Encoding A Human Dopamine D1
RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/168,510
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,267
FILING DATE: 05-OCT-1993
APPLICATION NUMBER: 07/551,448
FILING DATE: 10-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 140..1573
US-09-168-510-1

Query Match 7.0%; Score 92.4; DB 3; Length 1771;

Best Local Similarity 51.4%; Pred. No. 7.4e-14;
Matches 213; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 247 CAGTGGCATTGACAGTCTGCTCCCTCAAGCTGGGACCTTCACGGTCTGGAGAACCTC 306
DB 257 CAGGTGTCACCGCTGCTGCTGTAACCTCATCATCTGAGACCTGCTGGGCAACGTG 316
QY 307 CTGTGCTGTGCTGCTCATCTCCGACGCTCCGCTGAGGCTTCTTCAACATTC 366
DB 317 CTGTGCTGTGCTGCTCATCTCCGACGCTCCGCTGAGGCTTCTTCAACATTC 376
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DB 377 ATCGTCTCTGGCCGTGTCAAGACCTTTTCGTGGCGCTGCTGTATGCTCCGGAAGCA 436
QY 427 GACTTCACAGTGTTCACCGCAAGATAGCCGCAAGTGTTCCTGTTCAAACTGGGTGG 486
DB 437 GTCCGCGAGGTGGCGGTACTGAGCCCTTTGAGAGGTCTGAGAGTCTGGGTGCTTC 496
QY 487 GTACAGGCTCTCTTCACTGCTCTCGTGGGACGCTGTTCTTCAAGCAATGACGTTAC 546
DB 497 GACATCATGTGCTCTCACTGCTCTCAATCTGAACTGTGTGCTCATGAGGTGACGCTAC 556
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QY 607 GCGTTTTCCTGATGTGACCATAGCATTTGATGCGCGTCTGCTCTCTG 660
DB 617 ATGTGCGGCTGTGAGGACCTTGTCTCATCTCTTCACTCCGCTCAG 670

RESULT 11
US-10-277-078-1

Sequence 1, Application US/10277078
Patent No. 6939680
GENERAL INFORMATION:
APPLICANT: Weishank, Richard L.
TITLE OF INVENTION: DNA Encoding A Human Dopamine D1 Receptor And Uses Thereof
Hartig, Paul R.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/277,078
FILING DATE: 21-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/168,510
FILING DATE: <Unknown>
APPLICATION NUMBER: 07/969,267
FILING DATE: 05-Oct-1993
APPLICATION NUMBER: 07/551,448
FILING DATE: 10-Jul-1990
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 140..1573
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-277-078-1
Query Match 7.0%; Score 92.4; DB 3; Length 1771;
Best Local Similarity 51.4%; Pred. No. 7.4e-14;
Matches 213; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 247 CAGTGGCCATTGACGCTCTGCTCAACGCTGGGACCTTCACGGTCTGTGAGAACCTC 306
Db 257 CAGGTGTACCGCTGCTGCTGACCTACTCATCTGAGACCTGCTGGGCAACGTG 316
QY 307 CTGGGTGTGTGCTGCTATCTCTCACTCCGCGACCTCTCCGTGTGAGAGCTTCTTCAACACTTC 366
Db 317 CTGGGTGTGCGACGCTATGTGTGGAGCGCGACCTGTGGCGCCAAATGACCAACGCTTTC 376
QY 367 ATCGGACGCTGTGGCGGTGAGACCTCTGTGGGAGTGTCAATTTTGTCTAAGCTTCAAT 426
Db 377 ATCGGTGTCTGTGGCGGTGTGAGACCTTTTGTGGGCGCTGTGTATGCTCCGTGGAAGCA 436
QY 427 GACTTCAACGTGTTCACCGCAAGATAGCGCAACGTGTTCCTTCAAACTGGGTGGG 486
Db 437 GTCCGCGAGGTGGCGGTACTGTGCGCTTTGGAGAGTTCGTGACGCTCGGGGTGCGCTTC 496

QY 487 GTACAGGCTCTCTTCACTGCTCCGTGGGACGCTGTTCCTCAAGCCATTCAGAGAGTAC 546
Db 497 GACATCATGTGTCTCACTGCTCTTCACTCCGAACTGTGTGTATCATAGCTGAGACCGCTAC 556
QY 547 ATATCATTCACAGGCGCTGTGATTAAGAGATTGTACAGAGGCCCAAGCGCTGTGA 606
Db 557 TGGGCATCTCCAGGCGCTTCCGCTAACAGCGCAAGATGATCAAGCGCATGTGCGCTTGTGTC 616
QY 607 GCGTTTGGCTGATGTGAGCAATAGCATTTGATCGCGGTGCTGCTCTG 660
Db 617 ATGTGCGCTGTGAGCAATGACCTTGTTCATCTTCACTCTTCAATTCGGTTCAG 670

RESULT 12
US-09-826-509-492
Sequence 492, Application US/09826509
Patent No. 6806054
GENERAL INFORMATION:
APPLICANT: Lehmann-Brunsmma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
SEQ ID NO 492
LENGTH: 1434
TYPE: DNA
ORGANISM: Homo sapiens
US-09-826-509-492
Query Match 6.9%; Score 90.8; DB 3; Length 1434;
Best Local Similarity 51.2%; Pred. No. 1.8e-13;
Matches 212; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY 247 CAGTGGCCATTGACGCTCTGCTCAACGCTGGGACCTTCACGGTCTGTGAGAACCTC 306
Db 118 CAGGTGTACCGCTGCTGCTGACCTTCACTCATCTGAGACCTGCTGGGCAACGTG 177
QY 307 CTGGGTGTGTGCTGCTATCTCTCACTCCGCGACCTCCGCTGAGAGCTTCTTCAACACTTC 366
Db 178 CTGGGTGTGCGACGCTATGTGTGGAGCGCGCACCTGTGGCGCCAAATGACCAACGCTTTC 237
QY 367 ATCGGACGCTGTGGCGGTGAGACCTCTGTGGGAGTGTCAATTTTGTCTAAGCTTCAAT 426
Db 238 ATCGGTGTCTGTGGCGGTGTGAGACCTTTTGTGGGCGCTGTGTATGCTCCGTGGAAGCA 297
QY 427 GACTTCAACGTGTTCACCGCAAGATAGCGCAACGTGTTCCTTCAAACTGGGTGGG 486
Db 298 GTCCGCGAGGTGGCGGTACTGTGCGCTTTGAGAGGTTCGACGCTGTGGGTGCGCTTC 357
QY 487 GTACAGGCTCTCTTCACTGCTCCGTGGGAGAGCTGTTCCTCAACAGCCATGAGAGGTAC 546
Db 358 GACATCATGTGTCTCACTGCTCTTCACTCTGAACTGTGTGTATGATGAGTGAAGCGGATG 417
QY 547 ATATCATTCACAGGCGCTGTGATTAAGAGATTGTACAGAGGCCCAAGCGCTGTGA 606
Db 418 TGGGCATCTCCAGGCGCTTCCGCTAACAGCGCAAGATGATCAAGCGCATGTGCGCTTGTGTC 477
QY 607 GCGTTTGGCTGATGTGAGCAATAGCATTTGATCGCGGTGCTGCTCTCTG 660
Db 478 ATGTGCGCTGTGAGCAATGACCTTGTTCATCTTCACTTCGGTTCAG 531

RESULT 13
US-07-791-936A-1

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

[illegible]

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Title:          US-10-521-428A-1
Perfect score:  1320
Sequence:       1. atgaagtcgatactagatg.....cgtctgcgcgaggtctctgga 1320

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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1: GenEmbl: *
2:  gb_env: *
3:  gb_pat: *
4:  gb_ph: *
5:  gb_pl: *
6:  gb_pr: *
7:  gb_ro: *
8:  gb_sts: *
9:  gb_sy: *
10: gb_un: *
11: gb_vl: *
12: gb_ov: *
13: gb_in: *
14: gb_on: *
15: gb_ba: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1320	100.0	1320	2	CQ768746	CQ768746 Sequence
2	1320	100.0	1320	5	AY766182	AY766182 Homo sapi
3	1259.4	95.4	5665	2	CS242372	CS242372 Sequence
4	1259.4	95.4	5665	2	AX658255	AX658255 Sequence
5	1259.4	95.4	5665	2	AX818167	AX818167 Sequence
6	1259.4	95.4	5665	5	HSU71304	U73304 Human CBI C
7	1257.8	95.3	1419	5	AY225522	AY225522 Homo sapi
8	1257.8	95.3	1419	5	BC100968	BC100968 Homo sapi
9	1257.8	95.3	1419	5	BC100969	BC100969 Homo sapi
10	1257.8	95.3	1492	5	BC074811	BC074811 Homo sapi
11	1257.8	95.3	1492	5	BC074812	BC074812 Homo sapi
12	1257.8	95.3	1631	2	CQ755118	CQ755118 Sequence
13	1257.8	95.3	1755	2	CS207294	CS207294 Sequence
14	1257.8	95.3	1755	2	AX548798	AX548798 Sequence
15	1257.8	95.3	1755	2	AX548798	AX548798 Sequence
16	1257.8	95.3	5480	2	CS115070	X54937 Human mRNA
17	1257.8	95.3	5480	2	CS115070	CS115070 Sequence
18	1257.8	95.3	5480	2	DD187125	DD187125 Novel tar
19	1257.8	95.3	112122	5	AL136096	AL136096 Human DNA

19	1256.2	95.2	1419	2	CQ768994	Sequence
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21	1256.2	95.2	1419	5	BC100970	Homo sapi
22	1256.2	95.2	1419	5	BC100971	Homo sapi
23	1256.2	95.2	1419	5	DQ067455	Homo sapi
24	1256.2	95.2	2135	2	DD210209	Methods o
25	1256.2	95.2	2135	2	AR308087	Sequence
26	1256.2	95.2	2135	2	AR3080924	Sequence
27	1256.2	95.2	2135	2	HSCAN6	Sequence
28	1256.2	95.2	2135	7	G28592	human STS s
29	1254.6	95.0	1419	2	CQ768996	Sequence
30	1254.6	95.0	1419	2	AR591295	Sequence
31	1254.6	95.0	1419	2	AX208045	Sequence
32	1254.6	94.8	1443	5	AF107262	Homo sapi
33	1249.8	94.7	1419	5	AY995204	Homo sapi
34	1248.2	94.6	1419	5	AY655255	Pan trogl
35	1247.8	94.5	1415	5	BC095513	Homo sapi
36	1229.8	93.1	1419	5	AF268025	Macaca mu
37	1151	87.2	1252	2	CS115071	Sequence
38	1151	87.2	1252	2	DD187126	Novel tar
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40	1079.8	81.8	1419	14	FC094342	Felis catus
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43	1049.6	79.5	5465	6	RNSR6R	Rat mRNA fo
44	1048	79.4	1422	6	AF153345	Mus muscu
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ALIGNMENTS

[illegible]

Db	181	GAGAACATTCAGTGTGGGAGAACTTCAATGACATAGAGTGTTCATGTCTTGAACCCC	240
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Db	241	AGCCGACAGCTGGCCATTGACAGTCTGTGCTCCCTACGCTGGGACCTTCACGGTCTGGAG	300
Qy	301	AACCTCTGTGTGTGTGTGATCTCTCCATCTCCGACGCTTCCGTGACAGGCTTCTTAC	360
Db	301	AACCTCTGTGTGTGTGTGATCTCTCCATCTCCGACGCTTCCGTGACAGGCTTCTTAC	360
Qy	361	CACCTTCATCGGACGCTGGCGGTGGGACGCTCTGGGGAGTGCATTTTGTCTACAGC	420
Db	361	CACCTTCATCGGACGCTGGCGGTGGGACGCTCTGGGGAGTGCATTTTGTCTACAGC	420
Qy	421	TTCATTTGACTTCCAGGTGTTCCACGCAAGATAGCCGACAGTGTGTTCTGTCAAACCTG	480
Db	421	TTCATTTGACTTCCAGGTGTTCCACGCAAGATAGCCGACAGTGTGTTCTGTCAAACCTG	480
Qy	481	GGTGGGGGTCACGGCTCTCTTCACTGCTCTGGGGGACGCTGTCTCTACAGCATCGAC	540
Db	481	GGTGGGGGTCACGGCTCTCTTCACTGCTCTGGGGGACGCTGTCTCTCAACCATCGAC	540
Qy	541	AGGTACATATCCATTCACAGGCCCCGTGGCTTAAAGGATGTGACACAGGGCCAAAGGC	600
Db	541	AGGTACATATCCATTCACAGGCCCCGTGGCTTAAAGGATGTGACACAGGGCCAAAGGC	600
Qy	601	GTTGTAGCGTTTTGTGCTGATGTGACCAATAGCCATTTGATGCGCGTGTGCTCTCTG	660
Db	601	GTTGTAGCGTTTTGTGCTGATGTGACCAATAGCCATTTGATGCGCGTGTGCTCTCTG	660
Qy	661	GGCTGGAACTGCGAGAACTGCAATCTGTTTGCTCAGACATTTTCCACACATTTAGAA	720
Db	661	GGCTGGAACTGCGAGAACTGCAATCTGTTTGCTCAGACATTTTCCACACATTTAGAA	720
Qy	721	ACCTACCTGATGTTCGTGATGGGGGTACCAAGGATCTGTCTTGTTCATCGGTATGG	780
Db	721	ACCTACCTGATGTTCGTGATGGGGGTACCAAGGATCTGTCTTGTTCATCGGTATGG	780
Qy	781	TACATGTATATCTCTGGAAGGCTCACAGCCACGCGTCCGATGATTCAGCGTGGACCC	840
Db	781	TACATGTATATCTCTGGAAGGCTCACAGCCACGCGTCCGATGATTCAGCGTGGACCC	840
Qy	841	CAGAAAGCATCATCCACACGTCGAGAGTGAAGTGAAGTGAACCCGGCCAGAC	900
Db	841	CAGAAAGCATCATCCACACGTCGAGAGTGAAGTGAAGTGAACCCGGCCAGAC	900
Qy	901	CAGCCCCGATGACATTAGGTTAGCCAAAGCCCTGTCTGTATCTGTGTGTGTGAATC	960
Db	901	CAGCCCCGATGACATTAGGTTAGCCAAAGCCCTGTCTGTATCTGTGTGTGTGAATC	960
Qy	961	ATCTGCTGGGGGCTCTGCTTGCAATCAGGTGTATGATGTCTTTGGGAAAGTGAACAG	1020
Db	961	ATCTGCTGGGGGCTCTGCTTGCAATCAGGTGTATGATGTCTTTGGGAAAGTGAACAG	1020
Qy	1021	CTCATTTAAGACGGTGTTCATTTCTGACAGTATGCTCTGCTGTGAATCTCAACCGTGAAC	1080
Db	1021	CTCATTTAAGACGGTGTTCATTTCTGACAGTATGCTCTGCTGTGAATCTCAACCGTGAAC	1080
Qy	1081	CCCATCATTTATGCTCTGAGAGTGAAGACCTGCGACACGCTTTCGGAGCATGTTTCCC	1140
Db	1081	CCCATCATTTATGCTCTGAGAGTGAAGACCTGCGACACGCTTTCGGAGCATGTTTCCC	1140
Qy	1141	TCTTGTGAAGGACCTGCGAGGCTCTGGAATACAGATGGGGGACCTCGACCTGCGAC	1200
Db	1141	TCTTGTGAAGGACCTGCGAGGCTCTGGAATACAGATGGGGGACCTCGACCTGCGAC	1200
Qy	1201	AAACACGCAAAACATGACCCAGTGTTCACAGGGCCGACAGAAAGCTGCATCAAGACAG	1260
Db	1201	AAACACGCAAAACATGACCCAGTGTTCACAGGGCCGACAGAAAGCTGCATCAAGACAG	1260
Qy	1261	GTCAGAGTTGCCAAGGTAAACATGTCTGTGTCCACAGACGCTTCCAGAGCTCTGTGA	1320

DB	1261	GTCAAAGTTGCCAAGGTACCAATGCTGTCTGTCCACAAGCAGTCTGGCGGAGCTCTTGNGA	1320 bp
RESULT 2	AY766182	1320 bp	mRNA linear PRI 03-JAN-2005
LOCUS	AY766182		
DEFINITION	Homo sapiens cannabinoid receptor 1 splice variant Cblb mRNA,		
ACCESSION	complete cds, alternatively spliced.		
VERSION	AY766182		
KEYWORDS	AY766182.1 GI:54609769		
SOURCE	.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1320)		
AUTHORS	Ryberg,B., Vu,H.K., Larsson,N., Groblewski,T., Hjorth,S.,		
TITLE	Elstbring,T., Sjogren,S. and Greasley,P.J.		
JOURNAL	Identification and characterisation of a novel splice variant of		
PUBMED	the human Cblb receptor		
AUTHORS	FEBIS Lett. 579 (1), 259-264 (2005)		
TITLE	15620723		
JOURNAL	2 (bases 1 to 1320)		
PUBMED	Khang,Vu,H., Groblewski,T. and Greasley,P.		
AUTHORS	Direct Submission		
TITLE	Submitted (28-SEP-2004) Molecular Sciences, AstraZeneca, 7171		
JOURNAL	Frederick Banting, Saint-Laurent, QC H4S1Z9, Canada		
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	/map="6q14-q15"		
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	/product="cannabinoid receptor 1 splice variant Cblb"		
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	LLGNCKELIOSVGSDIPHDIDETIMPIGWTSVLIPTVAVAWYLAKASHAVRMDD		
	QRGOKSLTIITSDRGVOVTRPDQANDRIALATIVLILVVLLICWEPILAIVWDYD		
	FGKNKKLIKTFAPCSMCLLNSTVNPITYALRSKDRLMARSRPSPSEGRNQPLDNS		
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ORIGIN			
Query Match:	100.0%; Score 1320; DB 5; Length 1320;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1320; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
AY	1 ATGAAGTGCATCTAGATGGCTTGACAGATACCACCTTCGACACCATCACCATGACCTC	60	
DB	1 ATGAAGTGCATCTAGATGGCTTGACAGATACCACCTTCGACACCATCACCATGACCTC	60	
AY	61 CTGGGAAGTCCCTTCCAAGAGAAGTAGCTGGGGAGAACACCCCAGACTAGTCCACAGA	120	
DB	61 CTGGGAAGTCCCTTCCAAGAGAAGTAGCTGGGGAGAACACCCCAGACTAGTCCACAGA	120	
AY	121 GACCAAGTGAACATTACAGAAATTTTACAAACAAGTCTCTCTGCTCTTAAGAGAGATAG	180	
DB	121 GACCAAGTGAACATTACAGAAATTTTACAAACAAGTCTCTCTGCTCTTAAGAGAGATAG	180	
AY	181 GAGAACATCCAGTGTGGGGAGAACTTACATGACATAGAGTGTTCATGAGTCTGGAACCC	240	
DB	181 GAGAACATCCAGTGTGGGGAGAACTTACATGACATAGAGTGTTCATGAGTCTGGAACCC	240	
AY	241 AGCCAGCAGCTGGCCATTGACGTCTGTCTCAACGCTGGGACCTTACAGGTCTGTGANG	300	

Db	241	AGCCAGCAGCTGGCCATTGSCAATCTCTGTCCCTCAACGCTGGGACCTTCAACGCTCTGGAG	300
Qy	301	AACTCTCTGTGCTGTGCGCTCAATCCTCCACATCCCGCAGCCTTCGCTGACAGGCTTCTTAC	360
Db	301	AACTCTCTGTGCTGTGCGCTCAATCCTCCACATCCCGCAGCCTTCGCTGACAGGCTTCTTAC	360
Qy	361	CACCTTCATCCGAGCCTGGCGGCTGGCAGACCTCTCTGGGAGAGTGCATTTTGTGTACACAC	420
Db	361	CACCTTCATCCGAGCCTGGCGGCTGGCAGACCTCTCTGGGAGAGTGCATTTTGTGTACACAC	420
Qy	421	TTCAATTGACCTTCCAGTGTTCCACCGCAAAAGATAGCCGCAAGCGTGTTCTGTCAAACTG	480
Db	421	TTCAATTGACCTTCCAGTGTTCCACCGCAAAAGATAGCCGCAAGCGTGTTCTGTCAAACTG	480
Qy	481	GGTGGGGGTCAACGCGCTCTTCACTGCTCCGTGGGAGCGCTGTCTCTCAACGCATTCGAC	540
Db	481	GGTGGGGGTCAACGCGCTCTTCACTGCTCCGTGGGAGCGCTGTCTCTCAACGCATTCGAC	540
Qy	541	AGGTACATATCCATTCAACAGGCCCCCGGCTGTAAAGAGATTGTCAACAGGCCCAAGGCTC	600
Db	541	AGGTACATATCCATTCAACAGGCCCCCGGCTGTAAAGAGATTGTCAACAGGCCCAAGGCTC	600
Qy	601	GTGGTAGCGTTTGTGCTGATGTGAGCAATAGGCATTGTGATGCGCGTGCTGCTCTCCG	660
Db	601	GTGGTAGCGTTTGTGCTGATGTGAGCAATAGGCATTGTGATGCGCGTGCTGCTCTCCG	660
Qy	661	GGCTGGAACTCGGAGAAACTGCAATCTGTTTCTCAGACATTTTCCACACATTGATGAA	720
Db	661	GGCTGGAACTCGGAGAAACTGCAATCTGTTTCTCAGACATTTTCCACACATTGATGAA	720
Qy	721	ACCTACCTGATGTTCTGATTCGAGGTCAACAGCGTACCTGCTTCTGTCAATCGGTATAGCG	780
Db	721	ACCTACCTGATGTTCTGATTCGAGGTCAACAGCGTACCTGCTTCTGTCAATCGGTATAGCG	780
Qy	781	TACATGTATATTTCTCTGGAAAGGCTCAACGCCACCGCTCCGATGATTAGGGTGGCAC	840
Db	781	TACATGTATATTTCTCTGGAAAGGCTCAACGCCACCGCTCCGATGATTAGGGTGGCAC	840
Qy	841	CAGAAAGACATCATCATCCACACGCTCTGAGATGGGAAGGTACAGGTGACCCGGCCAGAC	900
Db	841	CAGAAAGACATCATCATCCACACGCTCTGAGATGGGAAGGTACAGGTGACCCGGCCAGAC	900
Qy	901	CAAGCCGSCATGACATTAGGTTAGCCAAAGCCCTGTCTGATCCTGTGTGTGTTGATC	960
Db	901	CAAGCCGSCATGACATTAGGTTAGCCAAAGCCCTGTCTGATCCTGTGTGTGTTGATC	960
Qy	961	ATCTGCTGGGGCCCTCTGCTTGCAATCATGTGTATGATGTCTTTGGGAAGATGAACAG	1020
Db	961	ATCTGCTGGGGCCCTCTGCTTGCAATCATGTGTATGATGTCTTTGGGAAGATGAACAG	1020
Qy	1021	CTCATTTAAGACGSGTGTTCGATTTCTGACGATGATGCTCTGCTGAACTCCACCGTAAC	1080
Db	1021	CTCATTTAAGACGSGTGTTCGATTTCTGACGATGATGCTCTGCTGAACTCCACCGTAAC	1080
Qy	1081	CCCATCATCTATGCTCTGAGAGTAAAGACCTTGCGACACGCTTTCGAGACATGTTTCCC	1140
Db	1081	CCCATCATCTATGCTCTGAGAGTAAAGACCTTGCGACACGCTTTCGAGACATGTTTCCC	1140
Qy	1141	TCTTGTGAAGGACCTGCGCAGCTCTTGATTAACAGATGGGGAACTCGGACTGCTCGAC	1200
Db	1141	TCTTGTGAAGGACCTGCGCAGCTCTTGATTAACAGATGGGGAACTCGGACTGCTCGAC	1200
Qy	1201	AAACACGCAAAACAATGACGACGATTTCAACAGGCGCGCAAAAGCTGATCAAGAGCACG	1260
Db	1201	AAACACGCAAAACAATGACGACGATTTCAACAGGCGCGCAAAAGCTGATCAAGAGCACG	1260
Qy	1261	GTCAAGATTGGCCAAAGTAAACCATGTCTGTGTCCACAGACACGTCTGCCGAGGCTCTGTGA	1320
Db	1261	GTCAAGATTGGCCAAAGTAAACCATGTCTGTGTCCACAGACACGTCTGCCGAGGCTCTGTGA	1320

[illegible]

QY	712	ATTGATGAACCTACCTGATGTTCTGGAATCGGGGTACACAGCGTACTGCTTCTGTTCAATC	771
Db	932	ATTGATGAAACTTACCTGATGTTCTGGAATCGGGGTACACAGCGTACTGCTTCTGTTCAATC	991
QY	772	GTGATGCGTACATGATATATTTCTCGGAAGGCTCACAGCACGGCGTCCGATGATTTAG	831
Db	992	GTGATGCGTACATGATATATTTCTCGGAAGGCTCACAGCACGGCGTCCGATGATTTAG	1051
QY	832	CGTGGCACTCCAGAAGAGCATCATCTCAACACGCTCGAGATGGAGAGTACAGGTGAC	891
Db	1052	CGTGGCACTCCAGAAGAGCATCATCTCAACACGCTCGAGATGGAGAGTACAGGTGAC	1111
QY	892	CGGCGAGACCAAGCCCCGATGAGCATTTAGTGTAGCCAAAGACCTTGCTCTGATCTCGTG	951
Db	1112	CGGCGAGACCAAGCCCCGATGAGCATTTAGTGTAGCCAAAGACCTTGCTCTGATCTCGTG	1171
QY	952	GGTGTGATCATCTGCTGGGGCCCTCTGCTGCAATCATGAGTATGATGTCCTTTGGGAG	1011
Db	1172	GGTGTGATCATCTGCTGGGGCCCTCTGCTGCAATCATGAGTATGATGTCCTTTGGGAG	1231
QY	1012	ATGAACAAGCTCATTAAGAAGCGGTGTTTGATCTCGACATGCTCTGCTGCTGAATCC	1071
Db	1232	ATGAACAAGCTCATTAAGAAGCGGTGTTTGATCTCGACATGCTCTGCTGCTGAATCC	1291
QY	1072	ACCGTGAACCCGATCATCTTATGCTCTGAGAGTAAAGACCTGCGACACGCTTTCGGAGC	1131
Db	1292	ACCGTGAACCCGATCATCTTATGCTCTGAGAGTAAAGACCTGCGACACGCTTTCGGAGC	1351
QY	1132	ATGTTTCCCTCTTGTGAAGAGCATGCGGACCTCTGATATACAGATGGGGATCTCGAC	1191
Db	1352	ATGTTTCCCTCTTGTGAAGAGCATGCGGACCTCTGATATACAGATGGGGATCTCGAC	1411
QY	1192	TGCTGTCAACAACGCAAAACATGACAGCCAGTGTTCACAGGGCCGCAAGAACTGCATC	1251
Db	1412	TGCTGTCAACAACGCAAAACATGACAGCCAGTGTTCACAGGGCCGCAAGAACTGCATC	1471
QY	1252	AAGAGCAGCGTCAAGATTGCCAAGGTAAACATGTCTGTGTCCACAGACACGCTTGCCGAG	1311
Db	1472	AAGAGCAGCGTCAAGATTGCCAAGGTAAACATGTCTGTGTCCACAGACACGCTTGCCGAG	1531
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Db	1532	GCTCTGTGA 1540	
RESULT 4			
LOCUS	AX658255	5665 bp	DNA linear PAT 22-MAR-2003
DEFINITION	Sequence 171 from Patent WO03000928.		
ACCESSION	AX658255		
VERSION	AX658255.1	GI:29160783	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homidae; Homo.		
	1		
AUTHORS	Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,		
	Peterson,M.W. and Elisner,H.I.		
TITLE	Methods for identification of cancer cell surface molecules and		
	cancer specific promoters, and therapeutic uses thereof		
JOURNAL	Patent: WO 03000928-A 171 03-JUN-2003;		
	Odin Medical A/S (DK)		
FEATURES	Location/Qualifiers		
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ORIGIN	/db_xref="taxon:9606"		

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QY	112	GTCCAGCAGACCAAGGTGA	CATTACAGAAATTTTACACAAGTCTCTGCTCTTCAAG	171				
Db	332	GTCCAGCAGACCAAGGTGA	CATTACAGAAATTTTACACAAGTCTCTGCTCTTCAAG	391				
QY	172	GAGAAATAGAGGAACATCAGTGTGGGGGAA	CTTACATGACATAGAGTGTTCATGTC	231				
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QY	232	CTGAACCCCAAGCCAGACAGCTGCGCATTTGCAAGTCTGCTCCACAGCTGGACCTTTCACG	291					
Db	452	CTGAACCCCAAGCCAGACAGCTGCGCATTTGCAAGTCTGCTCCACAGCTGGACCTTTCACG	511					
QY	292	GTCTGTGAGAACTCTCTGTGCTGTGGCTATCTCTCACTTCGCGAGCTTCGCTGACAG	351					
Db	512	GTCTGTGAGAACTCTCTGTGCTGTGGCTATCTCTCACTTCGCGAGCTTCGCTGACAG	571					
QY	352	CCTTCCTACCACTTCATCGGACCTGGCGGTGGACACCTCCCTGGGAGGTGCATTTT	411					
Db	572	CCTTCCTACCACTTCATCGGACCTGGCGGTGGACACCTCCCTGGGAGGTGCATTTT	631					
QY	412	GTCTACAGCTTCATTGA	CTTCAAGTGTCCACGCAAAAGATACCCCAAGTGTTCG	471				
Db	632	GTCTACAGCTTCATTGA	CTTCAAGTGTTCACGCAAAAGATACCCCAAGTGTTCG	691				
QY	472	TTCAAACTGGGTGGGTGACGCGCTCTTCACTGCTCTCCGTGGGACCTGTTCACACA	531					
Db	692	TTCAAACTGGGTGGGTGACGCGCTCTTCACTGCTCTCCGTGGGACCTGTTCACACA	751					
QY	532	GCCATCGACAGTACATATCCATTCCACAGGCCCTTGGCCTATAGAGATTTGTACACAG	591					
Db	752	GCCATCGACAGTACATATCCATTCCACAGGCCCTTGGCCTATAGAGATTTGTACACAG	811					
QY	592	CCCAAGGCGGTGATAGCGTTTGTGCTGATGACCAATAGCCATTGTATGCGCGTGTG	651					
Db	812	CCCAAGGCGGTGATAGCGTTTGTGCTGATGACCAATAGCCATTGTATGCGCGTGTG	871					
QY	652	CCTCTCTCTGGGCTGGAACCTGCGAAGAACTGCAATCTGTTTGTCTCAGACATTTTCCACAC	711					
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QY	712	ATTGATGAACCTTACCTGATGTTTCTGGATCGGGGTACACAGCGTATGCTTCTGTATC	771					
Db	932	ATTGATGAACCTTACCTGATGTTTCTGGATCGGGGTACACAGCGTATGCTTCTGTATC	991					
QY	772	GTGATGTGTGACATGTATATTCTGTGGAAGGCTCACAGCCAGTCCGATATTTCAG	831					
Db	992	GTGATGTGTGACATGTATATTCTGTGGAAGGCTCACAGCCAGTCCGATATTTCAG	1051					
QY	832	CGTGGCAACCCAGAGAGCATCATCTCACACGTCTGAGATGGAGAGTACAGAGTACC	891					
Db	1052	CGTGGCAACCCAGAGAGCATCATCTCACACGTCTGAGATGGAGAGTACAGAGTACC	1111					
QY	892	CGGCGACACCAAGCCCGCATGGA	CAATTAGTTAGCCAAAGCCTTGTCGTGATCTTGCTG	951				
Db	1112	CGGCGACACCAAGCCCGCATGGA	CAATTAGTTAGCCAAAGCCTTGTCGTGATCTTGCTG	1171				
QY	952	GTGTTGAACATCTGTGGGGCCCTGTGCTGCAATCAATGATGTATGATGCTTTGGGAG	1011					
Db	1172	GTGTTGAACATCTGTGGGGCCCTGTGCTGCAATCAATGATGTATGATGCTTTGGGAG	1231					
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Db	1232	ATGAACAAGCTCATTTAAGACGSGTGTTCATTTGACAGTATGCTGTGCTGCTGAACCTC	1291					
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Db 1472 AAGAGACGGTCAAGATTTGCAAGGTAACCATGTCTGTGTCCACAGACGCTGCGCAG 1531
Qy 1312 GCTCTGTGA 1320
Db 1532 GCTCTGTGA 1540

RESULT 5
AX818167
LOCUS AX818167 5665 bp DNA linear PAT 10-DEC-2003
DEFINITION Sequence 38 from Patent WO03068268.
ACCESSION AX818167
VERSION AX818167.1 GI:39723240
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1
AUTHORS Ek, S., Borrebaeck, C.A. and Ehinger, M.
TITLE Treatment of comma; diagnosis and imaging of disease
JOURNAL Patent: WO 03068268-A 38 21-AUG-2003;
BIOINVENT INTERNATIONAL AB (SE)
FEATURES
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Best Local Similarity 99.5%; Pred. No. 0;
Matches 1563; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 52 ACTGACCTCTGTGAAGTCCCTTCCAAAGAGATGAGCTGCGGAGAGCAACCCCGACGTA 111
Db 272 ACTTCTTTAGGGAGAGTCTCTTCCAAAGAGATGAGCTGCGGAGAGCAACCCCGACGTA 331
Qy 112 GTCCAGCAGACAGGTGAACATTAACAATTTTAAACAAGTCTCTGCTGCTTCAAG 171
Db 332 GTCCAGCAGACAGGTGAACATTAACAATTTTAAACAAGTCTCTGCTGCTTCAAG 391
Qy 172 GAGGATGAGAGAAACATCAAGTGTGGGAGAACTTATGAGCAATGAGTGTTCATGTC 231
Db 392 GAGGATGAGAGAAACATCAAGTGTGGGAGAACTTATGAGCAATGAGTGTTCATGTC 451
Qy 232 CTGAACCCGAGCAGAGCTGAGCATTGAGTCTGCTGCTGCTGAGCAGCTTCAAG 291
Db 452 CTGAACCCGAGCAGAGCTGAGCATTGAGTCTGCTGCTGCTGAGCAGCTTCAAG 511
Qy 292 GTCTGTGAGAACCTCTGT 351
Db 512 GTCTGTGAGAACCTCTGT 571
Qy 352 CTTTCTTACCACTTATCTGCGCAGCTGTGGGTGGGAGCACTCTGTGGGAGTGTCTATTTT 411
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ACCESSION U73304
VERSION U73304.1 GI:1657840
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Hominidae; Homo.
1 (bases 1 to 5665)
Hoehe, M.R., Caenazzo, L., Martinez, M.M., Hsieh, W.T., Modi, W.S.,
Gershon, E.S. and Bonner, T.I.
Genetic and physical mapping of the human cannabinoid receptor gene
to chromosome 6q14-q15
New Biol. 3 (9), 880-885 (1991)
1931832
JOURNAL
PUBMED
2 (bases 1 to 5665)
Bonner, T.I.
The coding exon of the human CB1 cannabinoid receptor
Unpublished
3 (bases 1 to 5665)
Bonner, T.I.
Direct Submission
Submitted (03-Oct-1996) Lab of Cell Biology, NIMH, Bldg. 36, Rm
3A-17, MSC 4090, Bethesda, MD 20892-4090, USA
JOURNAL
3A-17, MSC 4090, Bethesda, MD 20892-4090, USA
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1419)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hejeh, F.,
Dietchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Cavaan, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carancini, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mollahy, S.J., Bosak, S.A., McPwan, P.J.,
McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Hellon, E., Kettleman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Matra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
JOURNAL 2 (bases 1 to 1419)
PUBMED
REFERENCES
AUTHORS NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdpax11.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
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 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932
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 AUTHORS NIH MGC Project
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 Email: cgabs-remail.nih.gov
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 cDNA Library Preparation: Baylor Human Genome Sequencing Center
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
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 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdpax11.stanford.edu
 Dickson, M., Schmitz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

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 Query Match 95.3% Score 1257.8; DB 5; Length 1419;
 Best Local Similarity 99.4%; Pred. No. 0;
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PUBLISHED			
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TITLE			
JOURNAL			
REMARK			
COMMENT			

1492 bp mRNA linear PRI 16-AUG-2004
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BC074811
 BC074811.2 GI:50595691
 MGC.

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 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A. CDNA
 Generation and initial analysis of more than 15,000 full-length
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 2 (bases 1 to 1492)
 Director MGC Project.
 Direct Submission
 Submitted (25-JUN-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 4, 2004 this sequence version replaced gi:49901676.
 Contact: MGC help desk
 Email: gsabbs-remail.nih.gov
 Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
 Center
 CDNA Library Preparation: British Columbia Cancer Research Center
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
 Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Pihlu,
 Parveen Saeedi, UR Santos, Angelique Scherch, Ursula Skalska,
 Duane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jacque
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
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Query Match      95.3%; Score 1257.8; DB 5; Length 1492;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1462; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DEFINITION BC074812
ACCESSION BC074812
VERSION BC074812.2 GI:50960443
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Homidae; Homo.
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Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
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JOURNAL
PUBMED
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AUTHORS
TITLE
JOURNAL

REMARK
COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRBU Plate: 4 Row: G Column: 5.
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ORIGIN

Query Match 95.3%; Score 1257.8; DB 5; Length 1492;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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ACCESSION CO725118
VERSION CO725118.1 GI:42285975
KEYWORDS
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Homnidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanecons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 11052 06-SEP-2002;
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ORIGIN

Query Match 95.3%; Score 1257.8; DB 2; Length 1631;
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DEFINITION Sequence 2 from Patent WO2005109000.
ACCESSION CS207294
VERSION CS207294.1 GI:83413202
KEYWORDS
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Hominidae; Homo.
REFERENCE
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 2 17-NOV-2005;
Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
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ACCESSION AX548798
VERSION AX548798.1 GI:25813708
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Hominidae; Homo.
REFERENCE
AUTHORS Butner, G.C., Roush, C.L., and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
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JOURNAL Patent: WO 02061087-A 83 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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Best Local Similarity 99.4%; Pred. No. 0;
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REFERENCE  1
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  TITLE    Nucleotide sequence of a human cannabinoid receptor cDNA
  JOURNAL  Nucleic Acids Res. 18 (23), 7142 (1990)
  PUBMED   2263478
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  AUTHORS  Gerard,C.M., Mollereau,C., Vassart,G. and Parmentier,M.
  TITLE    Molecular cloning of a human cannabinoid receptor which is also
           expressed in testis
  JOURNAL  Biochem. J. 279 (Pt 1), 129-134 (1991)
  PUBMED   1718258
  REFNOTE  3 (bases 1 to 1755)
  AUTHORS  Gerard,C.
  TITLE    Direct Submission
  JOURNAL  Submitted (23-OCT-1990) Gerard C., IRIHBN, Campus Erasme, 808 v De
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  COMMENT  Data kindly reviewed (14-MAR-1991) by Gerard c.
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GenCore version 5.1.9
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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	245.2	18.6	1083	US-11-242-505A-2	Sequence 2, Appli
3	245.2	18.6	1790	US-11-242-505A-1	Sequence 1, Appli
4	60.8	4.6	1885	US-11-289-102-47	Sequence 47, Appli
5	56.8	4.3	1080	US-11-257-851A-74	Sequence 74, Appli
6	53.6	4.1	599	US-10-488-619-1656	Sequence 1656, Ap
7	53	4.0	1074	US-11-302-678-39	Sequence 39, Appli
8	53	4.0	1159	US-11-302-678-37	Sequence 37, Appli
9	49.6	3.8	975	US-11-257-851A-78	Sequence 78, Appli
10	49.6	3.8	1579	US-10-449-902-19945	Sequence 19945, A
11	49.6	3.8	1650	US-11-312-958-39	Sequence 39, Appli
12	49.4	3.7	5132	US-10-505-928-663	Sequence 663, Appli
13	48.2	3.7	2193	US-10-504-973-47	Sequence 47, Appli
14	48	3.6	48	US-10-521-428A-6	Sequence 6, Appli
15	46.4	3.5	1936	US-10-449-902-18998	Sequence 18998, A
16	45.4	3.4	1847	US-10-511-937-2881	Sequence 2881, Ap
17	44.6	3.4	2452	US-10-449-902-12977	Sequence 12977, A
18	44.2	3.3	891	US-11-257-851A-72	Sequence 72, Appli
19	43.6	3.3	951	US-11-257-851A-70	Sequence 70, Appli
20	43.4	3.3	1107	US-10-449-902-16261	Sequence 16261, A
21	43.2	3.3	843	US-10-449-902-5465	Sequence 5465, Ap
22	43	3.3	1895	US-10-449-902-11498	Sequence 11498, A
23	42.8	3.2	1857	US-10-449-902-21743	Sequence 21743, A
24	42.8	3.2	1876	US-10-449-902-24607	Sequence 24607, A
25	42.6	3.2	1985	US-10-449-902-8322	Sequence 8322, Ap

26	42.6	3.2	2042	US-10-449-902-7918	Sequence 7918, Ap
27	42	3.2	990	US-10-449-902-2071	Sequence 2071, Ap
28	42	3.2	999	US-10-449-902-24779	Sequence 24779, A
29	42	3.2	1023	US-10-449-902-11722	Sequence 11722, A
30	41.6	3.2	1097	US-10-504-973-52	Sequence 52, Appli
31	40.8	3.1	1323	US-11-302-678-42	Sequence 42, Appli
32	40.8	3.1	1984	US-11-302-678-40	Sequence 40, Appli
33	40.6	3.1	1039	US-10-449-902-3356	Sequence 3356, Ap
34	40.6	3.1	1152	US-11-304-129-35	Sequence 35, Appli
35	40.6	3.1	1323	US-10-505-928-380	Sequence 380, App
36	40.6	3.1	1052	US-11-312-958-5	Sequence 5, Appli
37	40.4	3.1	963	US-11-332-138-3	Sequence 3, Appli
38	40.4	3.1	1903	US-11-332-138-1	Sequence 1, Appli
39	40	3.0	243	US-11-341-151-5	Sequence 5, Appli
40	40	3.0	267	US-11-341-151-3	Sequence 3, Appli
41	40	3.0	1170	US-10-953-349-32139	Sequence 32139, A
42	40	3.0	2040	US-10-449-902-20293	Sequence 20293, A
43	39.8	3.0	1796	US-10-449-902-16132	Sequence 16132, A
44	39.6	3.0	1240	US-10-953-349-40034	Sequence 40034, A
45	39.4	3.0	1005	US-10-449-902-22331	Sequence 22331, A

ALIGNMENTS

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RESULT 1
US-10-521-428A-1
; Sequence 1, Application US/10521428A
; Publication No. US20060115816A1
; GENERAL INFORMATION:
; APPLICANT: Vn, Huy Khang
; APPLICANT: Groblewski, Thierry
; TITLE OF INVENTION: Splice Variant Cannabinoid Receptor (CB1B)
; FILE REFERENCE: ASZD-P01-750
; CURRENT APPLICATION NUMBER: US/10/521,428A
; PRIOR FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 0202240-8
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-521-428A-1

Query Match      100.0%; Score 1320; DB 6; Length 1320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCGATCTAGATGCGCTTGACAGATACCACTTCGCGACCATCAGCATGACCTC 60
DB 1 ATGAAGTCGATCTAGATGCGCTTGACAGATACCACTTCGCGACCATCAGCATGACCTC 60

QY 61 CTGGGAATGCTCTTCCTTCAGAGAGAGATGACTCGGGAGAGCAACCCCGACCTAGTCCAGCA 120
DB 61 CTGGGAATGCTCTTCCTTCAGAGAGAGATGACTCGGGAGAGCAACCCCGACCTAGTCCAGCA 120

QY 121 GACCAAGGGAACATTAAGAAATTTTAAACAAGTCTCTGCTCTTAAAGAGAAATAG 180
DB 121 GACCAAGGGAACATTAAGAAATTTTAAACAAGTCTCTGCTCTTAAAGAGAAATAG 180

QY 181 GAGAACATTCAGATGAGGAGAACTTCATGAGCATATAGATGTTTCATGATGCTGAAACCC 240
DB 181 GAGAACATTCAGATGAGGAGAACTTCATGAGCATATAGATGTTTCATGATGCTGAAACCC 240

QY 241 AGCCAGCAGCTGGCCATTCAGATGCTCTTCCTTCAGCGTCCAGCTTCGAGAG 300
DB 241 AGCCAGCAGCTGGCCATTCAGATGCTCTTCCTTCAGCGTCCAGCTTCGAGAG 300

QY 301 AACCTCCGCGGCTGCTGATCTCCATCCGCGGAGCCCTCGCTGAGGACCTTCCAC 360
DB 301 AACCTCCGCGGCTGCTGATCTCCATCCGCGGAGCCCTCGCTGAGGACCTTCCAC 360
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Db 301 AACCTGAGTGTGAGTCACTCCAGACGCTCCGCTGACAGGCTTCTTAC 360
Qy 361 CACTTCATCGAGAGCTGGCGGTGGCAGACCTTCTGGGAGTGTATTTTGTACAGC 420
Db 361 CACTTCATCGAGAGCTGGCGGTGGCAGACCTTCTGGGAGTGTATTTTGTACAGC 420
Qy 421 TTCATTGACTTCCAGTGTTCACCGCAAGATAGCCGCAAGTGTTCCTTCTTAACTG 480
Db 421 TTCATTGACTTCCAGTGTTCACCGCAAGATAGCCGCAAGTGTTCCTTCTTAACTG 480
Qy 481 GGTGGGATCGAGGCTCTCTTCACTGCTCCGTGGGAGCTGTCTTCTCAAGCCATCAG 540
Db 481 GGTGGGATCGAGGCTCTCTTCACTGCTCCGTGGGAGCTGTCTTCTCAAGCCATCAG 540
Qy 541 AGGTATCATTCATTCACAGGCGCTTGGCTTTAAGAGATGTGTACACAGGCGCCAAAGCC 600
Db 541 AGGTATCATTCATTCACAGGCGCTTGGCTTTAAGAGATGTGTACACAGGCGCCAAAGCC 600
Qy 601 GTGTAGAGCTTTGCTGTATGTGACATAGCCATTTGTATGCGCGTGTCTCTCTG 660
Db 601 GTGTAGAGCTTTGCTGTATGTGACATAGCCATTTGTATGCGCGTGTCTCTCTG 660
Qy 661 GGTGGAATCTGGAAGAACTGCAATCTGTCTGAGACATTTTCCACATTTATGAA 720
Db 661 GGTGGAATCTGGAAGAACTGCAATCTGTCTGAGACATTTTCCACATTTATGAA 720
Qy 721 ACCTACCTGATTTCTGTGATCGGGGTTCACAGCCATGCTCTTCTGTATCTGTATGCG 780
Db 721 ACCTACCTGATTTCTGTGATCGGGGTTCACAGCCATGCTCTTCTGTATCTGTATGCG 780
Qy 781 TACATGATATTTCTGTGAGGCTCAACAGCCAGCGCTCCGATGATTCAGGCTGAC 840
Db 781 TACATGATATTTCTGTGAGGCTCAACAGCCAGCGCTCCGATGATTCAGGCTGAC 840
Qy 841 CAGAAAGCATCATATCCACAGCTCTGAGATGGAAGTACAGGTGACCCGCGCAAGC 900
Db 841 CAGAAAGCATCATATCCACAGCTCTGAGATGGAAGTACAGGTGACCCGCGCAAGC 900
Qy 901 CAAAGCCGATGGAATTTAGTTAGCCAAAGACCTGTGTCTGTATCTGTGTGTGTATC 960
Db 901 CAAAGCCGATGGAATTTAGTTAGCCAAAGACCTGTGTCTGTATCTGTGTGTGTATC 960
Qy 961 ATCTGCTGGGCGCTCTGCTTCAATCATGATGTATGATCTTTTGGAGAAATGAA 1020
Db 961 ATCTGCTGGGCGCTCTGCTTCAATCATGATGTATGATCTTTTGGAGAAATGAA 1020
Qy 1021 CTCATTAGAAGCGTGTGATTCAGTATGCTCTGCTGTGAACTCCACCGTGAAC 1080
Db 1021 CTCATTAGAAGCGTGTGATTCAGTATGCTCTGCTGTGAACTCCACCGTGAAC 1080
Qy 1081 CCCATCATTTATGCTCTGAGAGTAAAGACCTGCGACAGCTTTCCGAGCATTTTCCC 1140
Db 1081 CCCATCATTTATGCTCTGAGAGTAAAGACCTGCGACAGCTTTCCGAGCATTTTCCC 1140
Qy 1141 TCTTGTGAAGGACCTGCGAGCTCTGATTAACAGATGAGGAGACTCGGACTGCTGAC 1200
Db 1141 TCTTGTGAAGGACCTGCGAGCTCTGATTAACAGATGAGGAGACTCGGACTGCTGAC 1200
Qy 1201 AAAACGCAAAATATGACAGCTGTTCACAGGCGCGCAAGAAAGCTGATCAAGAGCAG 1260
Db 1201 AAAACGCAAAATATGACAGCTGTTCACAGGCGCGCAAGAAAGCTGATCAAGAGCAG 1260
Qy 1261 GTCAAGATTGCGAAGTAACTATGCTGTGTTCACAGACAGCTGTGCGAGGCTCTGTGA 1320
Db 1261 GTCAAGATTGCGAAGTAACTATGCTGTGTTCACAGACAGCTGTGCGAGGCTCTGTGA 1320

RESULT 2
US-11-242-505A-2
; Sequence 2, Application US/11242505A
; Publication No. US2006009656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.

APPLICANT: Healy, Aileen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hemtological Disorders Using 232, 2059, 10630, 12848, 13875,
FILE OF INVENTION: 14355, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
CURRENT FILING DATE: 2005-10-03
CURRENT FILING DATE: 2005-10-03
PRIOR APPLICATION NUMBER: US/11/242, 505A
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2002-12-16
PRIOR FILING DATE: 2002-12-16
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1083
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (1083)
US-11-242-505A-2

Query Match 18.6%; Score 245.2; DB 7; Length 1083;
Best Local Similarity 55.9%; Pred. No. 2.4e-58;
Matches 537; Conservative 0; Mismatches 378; Indels 45; Gaps 2;

Qy 167 TCAAGAGATAGAGAGAACTCCAGTGTGGGAGAACTTCATGAGCATAGATGTTTCA 226
Db 17 TGAAGAGATAGAGAGAACTCCAGTGTGGGAGAACTTCATGAGCATAGATGTTTCA 76
Qy 227 TGTCTTGAACCCAGCAGAGCTGGCATGTGATGATCTTCTTCACTGCTGCTGCT 286
Db 77 TGTCTTGAAGTGTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 136
Qy 287 TCAAGCTTGTGAGAACTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 346
Db 137 TAAAGCTTGTGAGAACTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 196
Qy 347 GAAAGCTTGTGAGAACTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 406
Db 197 GAAAGCTTGTGAGAACTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 256
Qy 407 TTTTGTCTAAGCTTCAATGATCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 466
Db 257 TCTTGTCTAAGCTTCAATGATCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 316
Qy 467 TTTTGTCTAAGCTTCAATGATCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 526
Db 317 TCTTGTCTAAGCTTCAATGATCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 376
Qy 527 TCAAGCATGAGAGAGTATATTCATTCACAGGCGCTGCTGCTGCTGCTGCTGCTGCT 586
Db 377 TCAAGCATGAGAGAGTATATTCATTCACAGGCGCTGCTGCTGCTGCTGCTGCTGCT 436
Qy 587 CCAAGCCCAAGGCGGTGTGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 646
Db 437 CCAAGCCCAAGGCGGTGTGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 496
Qy 647 TGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
Db 497 TGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
Qy 707 CACATATGATGAACTTACCTGATGCTTGTGATGCTGATGCTGATGCTGATGCTGATGCT 766
Db 551 CACTGATCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
Qy 767 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 826
Db 611 GAATCATCATCACTATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 668

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OY 827 TTCAGCGTGACCCAGAGAGCATCATCCACGCTCTGAGATGGAGATACAG 886
DB 669 -----GTCGGCCACAGAGACAGG 691
OY 887 TGACCCGGCAGACCAAGCCCGCATGAGATTAGGTTAGCCAAAGACCTGTCTGATCC 946
DB 692 TCCAGGAATGAGCCCAATGAGGCTGATGTGAGGTTGGCCAAAGACCTTAGGGCTAGTG 751
OY 947 TGTGTGTGTGATCATCTCTGCGGCTCTGCTTGTCATCATGTGTATGATGCTTTTG 1006
DB 752 TGGCTGTCTCTCATCTGTGTGTTCCAGTGTGCGCCCTCATGCGCCACAGCCTGGCCA 811
OY 1007 GGAAGATGAACAAGCTATTAAAGAGGTTTGTCATTGTCAGTATGCTGCGCTGCTGA 1066
DB 812 CTACGCTCATGATACCAAGGTCAAGAGAGCCCTTGCTTTGCTTCATAGCTGTGCTATCA 871
OY 1067 ACTCCACCGTGAACCCCATCATCTATGCTCTGAGAGTAAGACCTGCGACAGCTTTCC 1126
DB 872 ACTCATGTGTCAACCTGTCTATGTCTTACGAGATGGAAGATCCGCTCCTGCGCC 931
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RESULT 3
US-11-242-505A-1
; Sequence 1, Application US/11242505A
; Publication No. US2006009656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: MP12001-288P1RCP10MINIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290, 078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1790
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-242-505A-1
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Query Match 18.6%; Score 245.2; DB 7; Length 1790;
Best Local Similarity 55.9%; Pred. No. 3.2e-58;
Matches 537; Conservative 0; Mismatches 378; Indels 45; Gaps 2;

OY 167 TCAAGAGATGAGAGAAATCCAGTGTGGGAGAACTTCAATGACATAGAGTGTTTA 226
DB 143 TGACAGAGATGAGCAATGCTCCAGAGATGGCTTGAATTCACACCTTAGAAGATTACA 202
OY 227 TGGTCTGTAACCCAGCCAGCAGCTGCGCATTTGACAGTCTGTCCTTCAGAGCTGGGACCT 286
DB 203 TGTATCTAGTGTGTCCCAAGAGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 262
OY 287 TCACGCTCTGAGAACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 346
DB 263 TAAAGTCCCTGAGAGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 322
OY 347 GAGAGCTTCTTACCACTTATCGAGAGCTGTGGGTGTGCACACCTCTCTGGGAGGTGA 406
DB 333 GGAAGCTCTTATACCTGTTCATTTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 382
OY 407 TTTTGTCTACAGCTTCAATTTGACTTCAAGTGTTCACCGCAAGATAGCCGCAAGTGT 466
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DB 383 TCTTTCATGACGCTTTTGAAATTTTCATGTTTTCCATGATGTGTGATTCGAAGCTGTCT 442
OY 467 TTTCTGTTAAACTGTGGTGGGTTCAGAGCTCTCTTCACTGSCCTCCGGGGCAGAGCTGTCC 526
DB 443 TCTCTGTGAAGATGGCAGCGTGAATGACCTTCAACAGCTCTGTGGGTAGCTCTCC 502
OY 527 TCACAGCATTCGACAGTACATATTCATTCACAGAGCCCTGTGCTTAAGAGATTTGA 586
DB 503 TGACCGCATTTACCGATATCTCTGCTGCGCTATTCACCTTCTTCAAGAGCTTGTCTA 562
OY 587 CCAGGCCCAAGGCGGTGAGGTTTGTGCTGATGTGACATATGACATTTGATGTGCGG 646
DB 563 CCCGTGAAGAGGCACTGTGATCCCTGGGATCATGTGGGTCTCTCAGACATGATCTCT 622
OY 647 TGTGCTCTCTCTGGGCTGTGAACCTGAGAACTGCATCTGTGTCTCAGACATTTTCC 706
DB 623 ACTCGCCCTCATGGAGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 676
OY 707 CACACATTTGATGAACCTTACCTGATGTTTGTGATCGGGGTGACAGAGTACTGTCTGT 766
DB 677 CACTGATCCCAATGACTACCTGTGAGCTGTGCTCTGTTCATGCGCTTCTCTTTTCCG 736
OY 767 TCATGTGTATGCGTATGATATTTCTGTGAGAGGCTTCACAGCCGCTCCGATGA 826
DB 737 GATCATTTACACCTATGAGGATGTTCTGTGAAGGCCCATGAGATGTGGCAGCTT-- 794
OY 827 TTCAGCGTGACCCAGAGAGCATCATCCACGCTCTGAGATGGAAGATGATCAGG 886
DB 795 -----GTCGGCCACAGAGCAGGAG 817
OY 887 TGACCCGGCAGACCAAGCCCGCATGAGACATTTAGTTAGCCAAAGACCTGTCTGATCC 946
DB 818 TCCAGGAATGAGCCCGATGAGGCTGTGATGTGAGGTTGCGCAAGACCTTAGGGCTAGT 877
OY 947 TGTGTGTGTGATCATCTCTGCGGCTCTGCTTGTGATCATGTGTATGATGTTCTTTTG 1006
DB 878 TGGCTGTGTCTCTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 937
OY 1007 GGAAGATGAACAAGCTCATTTAAGAGCGGTGTGCAATTTGCAATGCTCTGCTGTGA 1066
DB 938 CTACGCTCATGATACCAAGTCAAGAGAGGCTTGTGCTTGTGCTTGTGCTGTGCTCATCA 997
OY 1067 ACTCCACCGTGAACCCCATCATCTATGCTCTGAGAGTAAGACCGTGGGACAGGCTTTCC 1126
DB 998 ACTCATGTGTCAACCTGTCTATGTCTTACGAGATGGAAGATCCGCTCCTGCGCC 1057
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RESULT 4
US-11-289-102-47
; Sequence 47, Application US/11289102
; Publication No. US2006012151A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 47
; LENGTH: 1885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-289-102-47

Query Match 4.6%; Score 60.8; DB 7; Length 1885;
Best Local Similarity 49.5%; Pred. No. 3.1e-07;
Matches 186; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
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/ CURRENT FILING DATE: 2005-12-14
/ PRIOR APPLICATION NUMBER: US/10/345,680
/ PRIOR FILING DATE: 2003-01-16
/ PRIOR APPLICATION NUMBER: US 60/349,511
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/360,500
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/365,041
/ PRIOR FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US 60/374,063
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/403,468
/ PRIOR FILING DATE: 2002-08-14
/ PRIOR APPLICATION NUMBER: US 60/414,262
/ PRIOR FILING DATE: 2002-09-27
/ PRIOR APPLICATION NUMBER: US 60/419,986
/ PRIOR FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US 60/423,809
/ PRIOR FILING DATE: 2002-11-05
/ PRIOR APPLICATION NUMBER: US 60/429,797
/ PRIOR FILING DATE: 2002-11-26
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 39
/ LENGTH: 1074
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1074)
US-11-302-678-39
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Query Match 4.0%; Score 53; DB 7; Length 1074;
Best Local Similarity 44.8%; Pred. No. 3.4e-05;
Matches 246; Conservative 0; Mismatches 300; Indels 3; Gaps 1;

QY 277 CTGGGACCTTACAGGCTCTGGAACCTCCCTGGTGTGGTCACTCTCCACCTCCGC 336
DB 148 CTGGGAGCGGCACTTCCCTGGAACCTGGTGTGGTCACTCTCCACCTCCGTGACGC 207
QY 337 AGCCTCGGTGAGGCTTCTTCAACCTTCACTGAGCGCTGGGCGGCGGCAAGCTCTG 396
DB 208 ACCTTCAACCGGCTGCCCAACACCTGAGCATCATGCGGTCTCGGATGTCTGGTG 267
QY 397 ---GGAGTGTCACTTTTGTCTACAGCTTCACTTCAAGTGTTCACCGCAAGAT 453
DB 268 GCGGCGGTGTATGCGGCTGAGCCTGTGATGAGCTGTCCGGCGCGCTGGCAGCTA 327
QY 454 AGCCGCAAGTGTCTGTCTTCAAACTGGGTGGGTGACGCGCTCTTCACTGCTCCGTG 513
DB 328 GGTGGAGGCTGTGCGGCTTTGGAATCGGTGAGCTGTCTTGTGCAAGCGCAGCATC 387
QY 514 GGCAGCTGTCTCTCAACAGCATGACAGAGTACATATTCATTACAGGCGCTGGCTAT 573
DB 368 TGGAACTGAGCGGCATATGCTTGAACCGCTACTGTGTCAATACGCGCAATGAAATAC 447
QY 574 AAGAGATTTGTCAACGAGCGCCAAAGCCGTGTGAGCTTTTGCCTGATGTGAACATAGCC 633
DB 448 AGCTTCGAGCCGCAAGTGTCTTCAACGTATGATGCGCTCACTCCGCGCACTCTCC 507
QY 634 ATTGATGCGCGGTGTGCTCTCTCGGCGCTGGAAGTGGAGAACTGCAATCTGTTTCG 693
DB 508 GCTGTCACTTCTCTGCGCCCGCTGCTTTTGTGCTGGGGAAGACGTACTCTGAGGCAAC 567
QY 694 TCAGACATTTTCCACACATTTGATGAACCTTACCTGATGTTTGTGATCGGGGTCAACAG 753
DB 568 GAGGAGTGCAGAGTAAAGCGGAGGCTTCTTAAGCGCGTGTCTTCCACGCTAAGCGCTTC 627
QY 754 GTACTGCTTCTTCTATCTGTATGAGTATGATATATTTCTTGAAGGCTCAACAGCAAC 813
DB 628 TACTTCGCGCTGTGTGTGTCTTCTGTGATGGAAGATCTACAAAGGCTCCAGATTC 687
QY 814 GCGGTCCGC 822
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DB 688 CCGGTGGCC 696

RESULT 8
US-11-302-678-37
/ Sequence 37, Application US/1102678
/ Publication No. US20060088881A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Siles-Santiago, Imaculada
/ APPLICANT: Venkateswarlu, Karicheti
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: UNOLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
/ TITLE OF INVENTION: 641, 260, 55089, 21407, 42033, 4656, 62553, 302, 323,
/ FILE REFERENCE: MP102-012PRNM OMNI
/ CURRENT APPLICATION NUMBER: US/11/302,678
/ CURRENT FILING DATE: 2005-12-14
/ PRIOR APPLICATION NUMBER: US/10/345,680
/ PRIOR FILING DATE: 2003-01-16
/ PRIOR APPLICATION NUMBER: US 60/349,511
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/360,500
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/365,041
/ PRIOR FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US 60/374,063
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/403,468
/ PRIOR FILING DATE: 2002-08-14
/ PRIOR APPLICATION NUMBER: US 60/414,262
/ PRIOR FILING DATE: 2002-09-27
/ PRIOR APPLICATION NUMBER: US 60/419,986
/ PRIOR FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US 60/423,809
/ PRIOR FILING DATE: 2002-11-05
/ PRIOR APPLICATION NUMBER: US 60/429,797
/ PRIOR FILING DATE: 2002-11-26
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 37
/ LENGTH: 1159
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (64)...(1137)
US-11-302-678-37

Query Match 4.0%; Score 53; DB 7; Length 1159;
Best Local Similarity 44.8%; Pred. No. 3.5e-05;
Matches 246; Conservative 0; Mismatches 300; Indels 3; Gaps 1;

QY 277 CTGGGACCTTACAGGCTCTGGAACCTCCCTGGTGTGGTCACTCTCCACCTCCGC 336
DB 211 CTGGGAGCGGCACTTCCCTGGAACCTGGTGTGGTCACTCTCCACCTCCGTGACGC 270
QY 337 AGCCTCGGTGAGGCTTCTTCAACCTTCACTGAGCGCTGGGCGGCGGCAAGCTCTG 396
DB 271 ACCTTCAACCGGTGTCCCAACACCTGTGTGATGATGAGCGGTCTCGGATGTCTGGTG 330
QY 397 ---GGAGTGTCACTTTTGTCTTCAAGCTTCACTTCAAGTGTTCACCGCAAGAT 453
DB 331 GCGGCGGTGTATGCGGCTGAGCTGTGATGAGCTGTCCGGCGCGCTGGAGCTA 390
QY 454 AGCCGCAAGTGTCTGTCTTCAAACTGGGTGGGTGACGCGCTCTTCACTGCGCTCCGTG 513
DB 391 GGTGGAGGCTGTGCACTTTTGAATCGGTGACGCTGCTTTTGTGCAAGCGCAGCATC 450
QY 514 GGCAGCTGTCTCTCAACAGCATGACAGAGTACATATTCATTACAGGCGCTGGCTAT 573
DB 451 TGGAACTGAGCGGCATATGCTTGAACCGCTTACTGTGTCAATACGCGCAATGAAATAC 510
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QY	574	AAGAGGATTTGTACACGAGCCCAAGGCGGTGTATGCGTTTTCCTGTATGTGGACATATAGCC	633
Db	511	ACGCTCCGCAACCCGCAAGTGCCTTCTCAACGTCATATATGCGGTCTACCTGGGACTCTCC	570
QY	634	ATTGTGATGCGCCGTGCTGCCTCTCTCGAGGCTGTGAATCGGAGAAACTGCATCTGTTTGC	693
Db	571	GCTGTGATCTCTGTGGCCCGCTGTGCTTTTGTGTGGGAGAGAGCATCTGTAGGGGAGC	630
QY	694	TCAGACATTTTCCCAACATTTGATGAACAACCTCATCTTCTGTGANTGGGGCTCACAGC	753
Db	631	GAGGAGTGCACAGTAAAGCCGACAGCCTTCTCTACCGGTGTCTCCACCCGATGGCGCTTTC	690
QY	754	GTACGTCTTCGTTCATCTGTGTATGCGGTACATGTATATTCTGTGAAGGCTCACAGCAC	813
Db	691	TACCTGCGCGCTGTGTGTGTGTGCTCTTCGTGTACTGGAAGATCTCAAGAGGTGCGCAAGTTTC	750
QY	814	GCCGTCCGC	822
Db	751	GCGGTGGGC	759

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RESULT 9
US-11-257-851A-78
; Sequence 78, Application US/11257851A
; Publication No. US20060105951A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mark
; APPLICANT: Stojanovic-Susulic, Vedrana
; APPLICANT: O'Neil, Karyn
; APPLICANT: Huang, Chichi
; APPLICANT: Luo, Jeffrey
; TITLE OF INVENTION: Melanocortin Receptor Binding Mimetibodies, Compositions, Methods
; TITLE OF INVENTION: Uses
; FILE REFERENCE: CEN5080 USA NP
; CURRENT APPLICATION NUMBER: US/11/257,851A
; CURRENT FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: 60/621,960
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-257-851A-78

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Query Match	3.8%	Score 49.6;	DB 7;	Length 975;
Best Local Similarity	58.2%	Pred. No. 0.00028;		
Matches 107; Conservative	0;	Mismatches 74;	Indels 3;	Gaps 1;

OY	266	GTGTCCTCAGCGTGGGACACCTTCAGCGTCTGGAGAACTCCGTGGTGTGTATCC	325
Db	125	TGTTTCTACCTGTGGGTGCATCAGCCTCTTGGAGAACCTTGGTCATAGGGGCCATAG	184
OY	326	TCCACTCCCGAGCCTCCGCTGAGAGGCTTCTACACACTTCATCGGAGCGTGGCGAGTGG	385
Db	185	TGAAGAACAAAACTGCACCTCC--CCATGTACTCTTCGTGTGACGCTTGGCAGTGG	241
OY	386	CAGACCTCTGGGAGAGTGTCAATTTTGTCTACAGCTTCATTTGACCTTCAGCGTGTCCACC	445
Db	242	CGGACATGTGTGTAGCATGTGCAGTGGCTTGGGAGACATCACATCTTACTCTAACCA	301
OY	446	GCAA	449
Db	302	ACAA	305

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RESULT 10
US-10-449-902-19945
; Sequence 19945, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

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1  APPLICANT: National Institute of Agrobiological Sciences.
2  APPLICANT: Bio-oriented Technology Research Advancement Institution.
3  APPLICANT: The Institute of Physical and Chemical Research.
4  APPLICANT: Foundation for Advancement of International Science.
5  TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
6  FILE REFERENCE: MOA-A0205Y1-US
7  CURRENT APPLICATION NUMBER: US/10/449,902
8  CURRENT FILING DATE: 2003-05-29
9  PRIOR APPLICATION NUMBER: JP 2002-203269
10 PRIOR FILING DATE: 2002-05-30
11 PRIOR APPLICATION NUMBER: JP 2002-383870
12 PRIOR FILING DATE: 2002-12-11
13 NUMBER OF SEQ ID NOS: 56791
14 SOFTWARE: PatentIn Ver. 2.1
15 SEQ ID NO 19945
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Matches 182;	Conservative 0;	Mismatches 199;	Indels 3;	Gaps 1

QY	82	AAAGATGA	CTGGGGGAGACAA	CCCCAGTAGTCC	CGAGACGACGAGTGAACATTACAGAA	141
Db	682	AATGTGACATC	AGGCGGATACCA	TTTATGACCTTCTCA	CTCCCAACCCGATGSA	741
QY	142	TTTTACA	CAAGTCTCTCTCGTCTTCA	AGGAGATGAGAA	CATCAGTGTGGGAG	201
Db	742	ATCGACCA	GAATTTCTTCTCCCATGTCA	AAATCGAGGACAGCTA	CATGTGTGGCGGAC	801
QY	202	AACTTCATGA	CAATGAGTGTTCATG	TGCTTCAACCCGAGCAG--	CAGCTGGCATT	258
Db	802	GACTGCAT	CGCCGTGAAGACGG	CGTGGACAGTACG	CATCAAGTTCAACATGCGCAGC	861
QY	259	GCAGTCTGT	CCCTCAGCTGGGACCTTCA	ACGGCTGTGAGAA	AACTCTGTGTGCTGAC	318
Db	862	CAGCACA	CTTCATCAGGAGGTCA	CCCTGCATCTCCCGACGAGGCAT	GTATCGCGCTC	921
QY	319	GTCAATCT	CCCACTCCCGAGCCTCG	CTGCAGGCGCTTCTTCA	CACTTATCGGACGCTG	378
Db	922	GCGACGAG	AATGTCCGCGGCATTC	CGCACGCGCGCGCTG	GAACAAGTCCGCATTCAC	981
QY	379	GCGGTGG	CAGACCTTCCTGGGAGTGTCA	TTTTTGTCTCA	CAAGCTTCAATTGCACGCTG	438
Db	982	ACCGAGT	CGGCGCTCAGGATCA	AAGTCCGGCGGGGCGCGGCGCTTA	CGTCAAGGACGTG	1041
QY	439	TTCCAC	CGGCAAAGATGCGCGCAC	462		
Db	1042	TTCTGCT	CGCGGCTCAGCCTTCAC	1065		

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RESULT 11
US-11-312-958-39
; Sequence 39, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47114, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MP102-027P1RMONMIN
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20

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Db 766 TCCTTCGATGAGGAGTGAACCCCTATGTTGGCTGGAACAATCTGAGTGGGTGAGCGG 825
Qy 631 TGCTGACATATTTTCCACACATGTATGAACCTACCTGATTTCTGGATCGGGGTACC 750
Db 826 GCCTGGGAGACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 885
Qy 751 AGCCGACTGCTTCTGTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 810
Db 886 ATCAGCATGAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 945
Qy 811 CACGCGCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
Db 946 CTGATGCTCTCATCTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1005
Qy 871 GATGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 930
Db 1006 GTGTGGGCTCTCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1065
Qy 931 ACCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 990
Db 1066 TGCTGGGCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1125
Qy 991 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1050
Db 1126 TGCAATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1185
Qy 1051 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
Db 1186 TTCTCTCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1245
Qy 1111 CTGGAGCAGGCTTTCGGAGGAGGATG 1135
Db 1246 TTCGCGTCACTCTCTTAAGATTT 1270
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RESULT 14
US-10-521-428a-6
; Sequence 6, Application US/10521428A
; Publication No. US20060115816A1
; GENERAL INFORMATION:
; APPLICANT: Vu, Huy Khang
; APPLICANT: Groblewski, Thierry
; APPLICANT: Gressley, Peter
; TITLE OF INVENTION: Splice Variant Cannabinoid Receptor (CB1B)
; FILE REFERENCE: AS2D-P01-750
; CURRENT APPLICATION NUMBER: US/10/521,428A
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 0202240-8
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of oligonucleotide used to delete polynucleotides
; OTHER INFORMATION: encoding human CB1b receptor N-terminus
US-10-521-428a-6
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Query Match 3.6%; Score 48; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 40 CGACCATCACCACCTCTCTGGAGAGTCCCTTCCAGAGAGATG 87
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RESULT 15
US-10-449-902-19898
; Sequence 19898, Application US/10449902
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; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute for Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19898
; LENGTH: 1936
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK070238
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-19898
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Query Match 3.5%; Score 46.4; DB 6; Length 1936;
Best Local Similarity 49.2%; Pred. No. 0.003;
Matches 122; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
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Qy 297 GAGAACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 356
Db 525 GGTATCTCTCAACCGCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 584
Qy 357 CTACCTTCAATCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 416
Db 585 CTTCCGCTTCTTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 644
Qy 417 CAGCTTCAATGATCTTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 476
Db 645 CATGATCCCCCAGGCTCTTGGCTTACGCTTCAACTTCCCAATCAGAAATGCTTCCAGGC 704
Qy 477 ACTGGTGGGATCAAGGCTCTTCACTGCTTCCGTTGGGAGAGGCTGTTCTTCCAGCCAT 536
Db 705 CCAAGCAAGGATCAATGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 764
Qy 537 CGACAGGT 544
Db 765 GCTCAGGT 772
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Job time : 71 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2006, 23:47:50 ; Search time 1644 Seconds
(without alignments)
9865.985 Million cell updates/sec

Title: US-10-521-428a-1

Perfect score: 1320

Sequence: 1 atgaagtcgacccatgatcg...cgctcgccagggcctcgtcga 1320

Scoring table: IDENTITY NUC

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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1259.4	95.4	5665	US-10-764-425-72	Sequence 72, Appl
2	1259.4	95.4	5665	US-10-482-029-171	Sequence 171, App
3	1259.4	95.4	5665	US-10-851-667A-24	Sequence 24, Appl
4	1257.8	95.3	1419	US-10-029-386-24875	Sequence 24875, A
5	1257.8	95.3	1755	US-10-225-567A-83	Sequence 83, Appl
6	1257.8	95.3	1755	US-10-295-027-235	Sequence 235, App
7	1257.8	95.3	1755	US-11-127-877-2	Sequence 27, Appl
8	1257.8	95.3	5480	US-11-019-829-27	Sequence 27, Appl
9	1257.8	95.3	5653	US-10-208-408-52	Sequence 52, Appl
10	1256.2	95.2	1419	US-10-521-420-2	Sequence 2, Appl
11	1256.2	95.2	1419	US-10-521-420-3	Sequence 3, Appl
12	1256.2	95.2	2135	US-10-101-510-715	Sequence 715, App
13	1256.2	95.2	2135	US-10-305-720-1450	Sequence 1450, App
14	1256.2	95.2	2135	US-10-641-643-1469	Sequence 1469, App
15	1256.2	95.2	5651	US-10-101-510-409	Sequence 409, App
16	1254.6	95.0	1419	US-09-826-509-468	Sequence 468, App
17	1254.6	95.0	1419	US-10-925-095-468	Sequence 468, App

18	1254.6	95.0	1419	US-10-521-420-4	Sequence 4, Appl
19	1251.4	94.8	5472	US-10-295-027-237	Sequence 237, App
20	1209.8	91.7	1551	US-09-823-245A-513	Sequence 513, App
21	1151	87.2	1252	US-10-295-027-239	Sequence 239, App
22	1151	87.2	1252	US-11-019-829-28	Sequence 28, Appl
23	1049.2	79.5	5489	US-11-136-527-2129	Sequence 2129, App
24	795.8	60.3	993	US-11-128-061-837	Sequence 837, App
25	795.8	60.3	993	US-11-128-049-837	Sequence 837, App
26	506.2	38.3	600	US-11-128-061-4479	Sequence 4479, App
27	506.2	38.3	600	US-11-128-049-4479	Sequence 4479, App
28	498.4	37.8	500	US-10-029-386-11154	Sequence 11154, A
29	412	31.2	600	US-11-060-756-2219	Sequence 2219, App
30	412	31.2	600	US-11-060-756-2220	Sequence 2220, App
31	412	31.2	600	US-11-060-756-6491	Sequence 6491, App
32	412	31.2	600	US-11-060-756-6492	Sequence 6492, App
33	252.4	19.1	3715	US-10-330-773-929	Sequence 929, App
34	252.4	19.1	44617	US-10-330-773-928	Sequence 928, App
35	246.8	18.7	1906	US-10-330-773-932	Sequence 932, App
36	246.8	18.7	21906	US-10-330-773-931	Sequence 931, App
37	246.4	18.7	1776	US-10-851-667A-25	Sequence 25, Appl
38	245.2	18.6	1083	US-10-290-078-2	Sequence 2, Appl
39	245.2	18.6	1776	US-10-225-567A-85	Sequence 85, Appl
40	245.2	18.6	1790	US-10-290-078-1	Sequence 1, Appl
41	245.2	18.6	1790	US-10-305-720-1359	Sequence 1359, App
42	245.2	18.6	1790	US-10-641-643-1398	Sequence 1398, App
43	242.8	18.4	2926	US-11-136-527-3556	Sequence 3556, App
44	240.4	18.2	1083	US-09-826-509-470	Sequence 470, App
45	240.4	18.2	1083	US-10-925-095-470	Sequence 470, App

ALIGNMENTS

RESULT 1				
US-10-764-425-72				
Sequence 72, Application US/10764425				
Publication No. US20040146921A1				
GENERAL INFORMATION:				
APPLICANT: Bayer Pharmaceuticals Corporation				
APPLICANT: Eveleigh, Deepa				
APPLICANT: Bigwood, Douglas				
APPLICANT: Taylor, Ian				
TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE				
FILE REFERENCE: 5151				
CURRENT APPLICATION NUMBER: US/10/764,425				
PRIOR FILING DATE: 2004-01-23				
PRIOR APPLICATION NUMBER: 60/442,582				
PRIOR FILING DATE: 2003-01-24				
NUMBER OF SEQ ID NOS: 191				
SOFTWARE: PatentIn version 3.2				
SEQ ID NO 72				
LENGTH: 5665				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-10-764-425-72				
Query Match				
Best Local Similarity 95.4%; Score 1259.4; DB 8; Length 5665;				
Matches 1263; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
QY	52	ACTGACCTCTGGGAGGTCCTCCAGAGGAAGTATGGGGGAGAACCCCAAGCTA	111	
DB	272	ACTTCCTTTAGGGGAGGTCCTCCAGAGGAAGTATGGGGGAGAACCCCAAGCTA	331	
QY	112	GTCCGAGAGACGAGTGAATTAAGATTTTACAAAGTCTCTCGCTCTTCAAG	171	
DB	332	GTCCGAGAGACGAGTGAATTAAGATTTTACAAAGTCTCTCGCTCTTCAAG	391	
QY	172	GAGATGAGGAGAACATTCAGTGGGGGAGAACTTCATGACATAGAGTTCATGATC	231	
DB	392	GAGATGAGGAGAACATTCAGTGGGGGAGAACTTCATGACATAGAGTTCATGATC	451	
QY	232	CTGAACCCGACGAGCTGGCATTCGATCTGTCCTCAGCGTGGGACCTTACG	291	

Db 452 CTGAACCCACAGCAGAGCTGGSCATGTGAGTCTGTCCCTCAGCCCTGGGACCTTCAAG 511
Qy 292 GTCCCGAGGAACCTCTGGTGTGTGGCGTCAATCCCTCCACTCCCGAGACTCCGCTGCAG 351
Db 512 GTCCGAGGAACCTCTGGTGTGTGGCGTCAATCCCTCCACTCCCGAGACTCCGCTGCAG 571
Qy 352 CCTTCTCACTCACTTCACTGAGCAGCTGGCGGTGGAGAGCTCTGGGGAGTGTCAATTTT 411
Db 572 CCTTCTCACTCACTTCACTGAGCAGCTGGCGGTGGAGAGCTCTGGGGAGTGTCAATTTT 631
Qy 412 GTTACAGCTTCACTTCACTGAGTGTTCACCGCAAGATAGCCGCAAGTGTTCG 471
Db 632 GTCTACAGCTTCACTTCACTGAGTGTTCACCGCAAGATAGCCGCAAGTGTTCG 691
Qy 472 TTCAAACTGGGTGGGTCAAGCCCTCTTCACTGCTCCGTGGGAGAGCTGTCTTCA 531
Db 692 TTCAAACTGGGTGGGTCAAGCCCTCTTCACTGCTCCGTGGGAGAGCTGTCTTCA 751
Qy 532 GCCATCGACAGGTACATATCCATTCACAGGCCCTGGCCCTATPAGAGATTGTCAACAG 591
Db 752 GCCATCGACAGGTACATATCCATTCACAGGCCCTGGCCCTATPAGAGATTGTCAACAG 811
Qy 592 CCCAAGCCGTGTAGCGTTTTCCTGATGTGACCATAGCCATTGTGATGCGCGTGTG 651
Db 812 CCCAAGCCGTGTAGCGTTTTCCTGATGTGACCATAGCCATTGTGATGCGCGTGTG 871
Qy 652 CCTCTCCGTGGGTGGAACCTGGAGAACTGCAATCTGTTTGTCTGACATTTTCCACAG 711
Db 872 CCTCTCCGTGGGTGGAACCTGGAGAACTGCAATCTGTTTGTCTGACATTTTCCACAG 931
Qy 712 ATTGATGAACCTACCTGATGTTCGATCGGGGTCAACAGCGTACTGCTGTTCATC 771
Db 932 ATTGATGAACCTACCTGATGTTCGATCGGGGTCAACAGCGTACTGCTGTTCATC 991
Qy 772 GTGTATGCGTACATGTATTTCTGTGAAGGCTCAAGCCAGCCGTCCGATGATTCAG 831
Db 992 GTGTATGCGTACATGTATTTCTGTGAAGGCTCAAGCCAGCCGTCCGATGATTCAG 1051
Qy 832 CGTGGCACCCGAGAAAGATCATCATCAACGTCTGAGAGTGGAGTACAGGTGACC 891
Db 1052 CGTGGCACCCGAGAAAGATCATCATCAACGTCTGAGAGTGGAGTACAGGTGACC 1111
Qy 892 CGGCGACAGCAAGCCCGATGAGCATTTAGGTTAGCCAGAACCTCTGATCTGTG 951
Db 1112 CGGCGACAGCAAGCCCGATGAGCATTTAGGTTAGCCAGAACCTCTGATCTGTG 1171
Qy 952 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGTGTATGATGTCTTGGAG 1011
Db 1172 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGTGTATGATGTCTTGGAG 1231
Qy 1012 ATGAACAAGCTCATTAAGACGCTTTTGCATCTGCAATGATGCTGCTGTGAACCTC 1071
Db 1232 ATGAACAAGCTCATTAAGACGCTTTTGCATCTGCAATGATGCTGCTGTGAACCTC 1291
Qy 1072 ACCGTGAACCCCATCATATGCTCTGAGAGTAAAGACCTGCAACGCTTCCGAGC 1131
Db 1292 ACCGTGAACCCCATCATATGCTCTGAGAGTAAAGACCTGCAACGCTTCCGAGC 1351
Qy 1132 ATGTTTCCCTCTGTGAAGGCACTGCGAGCCTCTGATTAACAGATGAGGAGACTCGAG 1191
Db 1352 ATGTTTCCCTCTGTGAAGGCACTGCGAGCCTCTGATTAACAGATGAGGAGACTCGAG 1411
Qy 1192 TGCCGCGACAAACAGCAAAATGACAGCACTGTTCACAGGCCGCGCAAAAGCTGCATC 1251
Db 1412 TGCCGCGACAAACAGCAAAATGACAGCACTGTTCACAGGCCGCGCAAAAGCTGCATC 1471
Qy 1252 AAGAGCAGGTCAAGATTGCGCAAGGTAAACATGTCTGTGTCCACAGACAGCTGTCCAG 1311
Db 1472 AAGAGCAGGTCAAGATTGCGCAAGGTAAACATGTCTGTGTCCACAGACAGCTGTCCAG 1531
Qy 1312 GCTCTGTGA 1320
|||||

Db 1532 GCTCTGTGA 1540
RESULT 2
US-10-482-029-171
; Sequence 171, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FIDE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482, 029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
; LENGTH: 5665
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-029-171

Query Match 95.4%; Score 1259.4; DB 9; Length 5665;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1263; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 52 ACTGACCTCTGGGAGTCCCTTCCAGAGAAAGATGACTGGGAGCAACCCCAAGCTA 111
Db 272 ACTTCTTTAGGGAGATGCTCTTCCAGAGAGATGACTGGGAGCAACCCCAAGCTA 331
Qy 112 GTCCAGCAGACAGGTGAACATTACAGAAATTTTACAAAGTCTCTGCTCTCAAG 171
Db 332 GTCCAGCAGACAGGTGAACATTACAGAAATTTTACAAAGTCTCTGCTCTCAAG 391
Qy 172 GAGATGAGGAACATCCAGTGTGGGAGAACTTCAATGACATPAGATGTTTATGTC 231
Db 392 GAGATGAGGAACATCCAGTGTGGGAGAACTTCAATGACATPAGATGTTTATGTC 451
Qy 232 CTGAACCCCAAGCCAGAGCTGGCAATGCACTGCTCTTCCATCAGCTGGGACCTTCAAG 291
Db 452 CTGAACCCCAAGCCAGAGCTGGCAATGCACTGCTCTTCCATCAGCTGGGACCTTCAAG 511
Qy 292 GTCTGAGGAACCTCTGTGTGTGTGCTCATCTCCAGAGCTTCGCTGTCAGG 351
Db 512 GTCTGAGGAACCTCTGTGTGTGTGCTCATCTCCAGAGCTTCGCTGTCAGG 571
Qy 352 CCTTCTTACCACTTATGTGGAGAGCTGGCGGTGGCAACCTCTGGGAGTGTCAATTTT 411
Db 572 CCTTCTTACCACTTATGTGGAGAGCTGGCGGTGGCAACCTCTGGGAGTGTCAATTTT 631
Qy 412 GTTACAGCTTCACTTGAACCTTCAAGTGTTCACCGCAAAAGATAGCCGCAAGTGTTCG 471
Db 632 GTTACAGCTTCACTTGAACCTTCAAGTGTTCACCGCAAAAGATAGCCGCAAGTGTTCG 691
Qy 472 TTCAAACTGGGTGGGTCAAGCCCTCTTCACTGCTCCGTGGGAGATTGTCAACAG 531
Db 692 TTCAAACTGGGTGGGTCAAGCCCTCTTCACTGCTCCGTGGGAGATTGTCAACAG 751
Qy 532 GCCATCGACAGGTACATATCCATTCACAGGCCCTGTGCTTAAAGAGATTGTCAACAG 591
Db 752 GCCATCGACAGGTACATATCCATTCACAGGCCCTGTGCTTAAAGAGATTGTCAACAG 811
Qy 592 CCCAAGCCGTGTAGCGTTTTCCTGATGTGAGCAATAGCCATTGTGATGCGCGTGTG 651
Db 812 CCCAAGCCGTGTAGCGTTTTCCTGATGTGAGCAATAGCCATTGTGATGCGCGTGTG 871
Qy 652 CCTCTCTGGGTGGAACCTGGAGAACTGCAATCTGTTTGTCTGACATTTTCCACAG 711
Db 872 CCTCTCTGGGTGGAACCTGGAGAACTGCAATCTGTTTGTCTGACATTTTCCACAG 931
Qy 712 ATTGATGAACCTACCTGATGTTCGATCGGGGTCAACAGCGTACTGCTGTTCATC 771
Db 932 ATTGATGAACCTACCTGATGTTCGATCGGGGTCAACAGCGTACTGCTGTTCATC 991
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QY 772 GTGATGCTACATGATATATCTCTGGAAGGCTCACAGCCAGCCGTCGCGATGATTGAG 831
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Db 992 GTGTATGGCTACATGATATTTCTCTGGAAGGCTCACAGCCAGCCGTCGCGATGATTGAG 1051
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QY 832 CGTGGACCCAGAAAGCATCATCATCCACAGCTGAGAGATGGGAAGGTACAGGTGACC 891
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Db 1052 CGTGGACCCAGAAAGCATCATCATCCACAGCTGAGAGATGGGAAGGTACAGGTGACC 1111
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|
|
QY 892 CGGCGACGACGAGCCGCGATGAGCAATTAAGGTAGCCAGAACCCCTGGTCTGTATCTCTGGAG 951
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|
Db 1112 CGGCGACGACGAGCCGCGATGAGCAATTAAGGTAGCCAGAACCCCTGGTCTGTATCTCTGGAG 1171
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|
|
QY 952 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGTGTATGATGTCTTTGGGAAG 1011
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|
|
Db 1172 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGTGTATGATGTCTTTGGGAAG 1231
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|
|
QY 1012 ATGAACAAGCTCATTAAGACGGGTGTTTGCAATCTGCAAGTATGCTGCTGCTGCAACTCC 1071
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|
|
Db 1232 ATGAACAAGCTCATTAAGACGGGTGTTTGCAATCTGCAAGTATGCTGCTGCTGCAACTCC 1291
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|
|
QY 1072 ACCGTGAACCCCATCATCTATGCTCTGAGAGATAGAGACCTGCGACAGCTTTCCGAGAC 1131
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Db 1292 ACCGTGAACCCCATCATCTATGCTCTGAGAGATAGAGACCTGCGACAGCTTTCCGAGAC 1351
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|
|
QY 1132 ATGTTCCCTCTTGTGAAGGCACTGCGAGCCCTCTGAGATTAAGAGATGGGGGACTCGAGC 1191
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Db 1352 ATGTTCCCTCTTGTGAAGGCACTGCGAGCCCTCTGAGATTAAGAGATGGGGGACTCGAGC 1411
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|
QY 1192 TGCTGCAAAACACGCAAAACATGACAGCCAGTGTTCACAGGGCCGCGAAAGCTGCATC 1251
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|
|
Db 1412 TGCTGCAAAACACGCAAAACATGACAGCCAGTGTTCACAGGGCCGCGAAAGCTGCATC 1471
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|
|
QY 1252 AAGGACAGGTCAGATGTCGCAAGGTAAACATGTCTGTCTCCAGACAGCTTCCGAG 1311
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|
|
Db 1472 AAGGACAGGTCAGATGTCGCAAGGTAAACATGTCTGTCTCCAGACAGCTTCCGAG 1531
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|
QY 1312 GCTCTGTGA 1320
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Db 1532 GCTCTGTGA 1540
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RESULT 3
US-10-851-667A-24

Sequence 24, Application US/10851667A
Publication No. US20050260608A1
GENERAL INFORMATION:
APPLICANT: Zimmer, Andreas
APPLICANT: Karsak, Meliha
APPLICANT: de Vernejoul, Marie-Christine
APPLICANT: Bab, Itai
APPLICANT: Shoham, Esther
APPLICANT: Mechoulam, Raphael
TITLE OF INVENTION: METHODS, KITS AND PHARMACEUTICAL COMPOSITIONS FOR DIAGNOSING,
TITLING OR INVENTION: DELAYING ONSET OF, PREVENTING AND/OR TREATING OSTEOPOROSIS
FILE REFERENCE: 28030
CURRENT APPLICATION NUMBER: US/10/851,667A
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24
LENGTH: 5665
TYPE: DNA
ORGANISM: Homo sapiens
US-10-851-667A-24

Query Match 95.4%; Score 1259.4; DB 10; Length 5665;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1263; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 52 ACTGACCTCTGGAAGTCCCTTCCAGAGAAAGTGAAGTGGGAGAGACACCCCAAGCTA 111
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|
Db 272 ACTTCTTTTGGGGAGTCCCTTCCAGAGAAAGTGAAGTGGGAGAGACACCCCAAGCTA 331
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|
|

QY 112 GTCCAGACGACAGGTGAACATTAACAAATTTTAAACAAGTCTCTCGCTTCAAG 171
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|
|
Db 332 GTCCAGACGACAGGTGAACATTAACAAATTTTAAACAAGTCTCTCGCTTCAAG 391
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QY 172 GAGAAATGAGAGAAACATCAAGTGGGGAGAACTTCAATGACATAGAGTGTTCATGTC 231
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|
|
Db 392 GAGAAATGAGAGAAACATCAAGTGGGGAGAACTTCAATGACATAGAGTGTTCATGTC 451
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|
|
QY 232 CTGAACCCCAAGCAGCAGCTGGCCATTTGCAAGTCTGTCTCTCAAGCTGGGACCTTCAAG 291
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|
|
Db 452 CTGAACCCCAAGCAGCAGCTGGCCATTTGCAAGTCTGTCTCTCAAGCTGGGACCTTCAAG 511
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|
|
QY 292 GTCCAGAGAACTCTCTGTGTGTGAGTCAATCTTCCACTCCGAGAGCTCCGCTGAG 351
|
|
|
Db 512 GTCCAGAGAACTCTCTGTGTGTGAGTCAATCTTCCACTCCGAGAGCTCCGCTGAG 571
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|
|
QY 352 CTTTCTTCAACTTTCATGCGAGCCCTGCGAGAGAGCTCTCTGGGAGTGTCAATTTT 411
|
|
|
Db 572 CTTTCTTCAACTTTCATGCGAGCCCTGCGAGAGAGCTCTCTGGGAGTGTCAATTTT 631
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|
|
QY 412 GTTACAGCTTCAATTAAGCTTCAAGTGTTCACCGCAAAAGATAGCCGCAAGTGTTCG 471
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|
|
Db 632 GTTACAGCTTCAATTAAGCTTCAAGTGTTCACCGCAAAAGATAGCCGCAAGTGTTCG 691
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|
|
QY 472 TTCAAACTGGGTGGGTGACAGGCTCTTCACTGCTCTCGTGGGAGAGCTGTCTTCA 531
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|
|
Db 692 TTCAAACTGGGTGGGTGACAGGCTCTTCACTGCTCTCGTGGGAGAGCTGTCTTCA 751
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|
QY 532 GCATCGACAGGTATCATATTCATTCACAGGCCCCCTGAGCTTAAAGAGATGTTCACAG 591
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Db 752 GCATCGACAGGTATCATATTCATTCACAGGCCCCCTGAGCTTAAAGAGATGTTCACAG 811
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|
QY 592 CCCAAGGCCGTGTAGCTTGTTCCTGTATGTGACCAATAGCCATTTGTATGCGCTGTG 651
|
|
|
Db 812 CCCAAGGCCGTGTAGCTTGTTCCTGTATGTGACCAATAGCCATTTGTATGCGCTGTG 871
|
|
|
QY 652 CCTCTCTGGGCTGGAACTGGAGAAACTGGAATCTGTTTCTCAGACATTTTCCACAC 711
|
|
|
Db 872 CCTCTCTGGGCTGGAACTGGAGAAACTGGAATCTGTTTCTCAGACATTTTCCACAC 931
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|
|
QY 712 ATTGATGAACCTTACCTGATGTTCTGATCGGGGTACACAGCTACTCTTCTGTTCATC 771
|
|
|
Db 932 ATTGATGAACCTTACCTGATGTTCTGATCGGGGTACACAGCTACTCTTCTGTTCATC 991
|
|
|
QY 772 GTGTATGCTGATGATATTTCTCTGGAAGCTCACAGCCAGCCGCTCGCATATTCAG 831
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|
|
Db 992 GTGTATGCTGATGATATTTCTCTGGAAGCTCACAGCCAGCCGCTCGCATATTCAG 1051
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|
|
QY 832 CGTGGACCCAGAAAGCATCATCATCCACAGCTGAGAGATGGGAAGGTACAGGTGACC 891
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|
|
Db 1052 CGTGGACCCAGAAAGCATCATCATCCACAGCTGAGAGATGGGAAGGTACAGGTGACC 1111
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|
|
QY 892 CGGCGACGACGAGCCGCGATGAGCAATTAAGGTAGCCAGAACCCCTGGTCTGTATCTCTGGAG 951
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|
|
Db 1112 CGGCGACGACGAGCCGCGATGAGCAATTAAGGTAGCCAGAACCCCTGGTCTGTATCTCTGGAG 1171
|
|
|
QY 952 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGTGTATGATGTCTTTGGGAAG 1011
|
|
|
Db 1172 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGTGTATGATGTCTTTGGGAAG 1231
|
|
|
QY 1012 ATGAACAAGCTCATTAAGACGGGTGTTTGCAATCTGCAAGTATGCTGCTGCTGCAACTCC 1071
|
|
|
Db 1232 ATGAACAAGCTCATTAAGACGGGTGTTTGCAATCTGCAAGTATGCTGCTGCTGCAACTCC 1291
|
|
|
QY 1072 ACCGTGAACCCCATCATCTATGCTCTGAGAGATAGAGACCTGCGACAGCTTTCCGAGAC 1131
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|
|
Db 1292 ACCGTGAACCCCATCATCTATGCTCTGAGAGATAGAGACCTGCGACAGCTTTCCGAGAC 1351
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|
|
QY 1132 ATGTTCCCTCTTGTGAAGGCACTGCGAGCTCTGAGATTAAGAGATGGGGGACTCGAGC 1191
|
|
|
Db 1352 ATGTTCCCTCTTGTGAAGGCACTGCGAGCTCTGAGATTAAGAGATGGGGGACTCGAGC 1411
|
|
|
QY 1192 TGCTGCAAAACACGCAAAACATGACAGCCAGTGTTCACAGGGCCGCGAAAGCTGCATC 1251
|
|
|

Db 1412 TGCCTGCAAAACGCAAAATGACAGCTGTTCAAGGCGCGCAAAAAGCTGATC 1471
Qy 1252 AAGAGCAGGTCAAGATTGCCAAGGTAAACATGTCTGTCTCAGACAGACGTCTGCCGAG 1311
Db 1472 AAGAGCAGGTCAAGATTGCCAAGGTAAACATGTCTGTCTCAGACAGACGTCTGCCGAG 1531
Qy 1312 GCTCTGTGA 1320
Db 1532 GCTCTGTGA 1540

RESULT 4

US-10-029-386-24875
; Sequence 24875, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEWOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24875
; LENGTH: 1419
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL136096.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.22
; OTHER INFORMATION: SWISSPROT HIT: P21554, EVALU0.00e+00
; OTHER INFORMATION: NT HIT: G16173524, EVALU0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: M7952.1, EVALU0.00e+00
US-10-029-386-24875

Query Match 95.3%; Score 1257.8; DB 7; Length 1419;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 52 ACTGACCTCTGGGGAAGTCCCTTCCAGAGATGACCTGCGGAGACAAACCCGAGCTA 111
Db 151 ACTTCTTTAGGGGAAGTCCCTTCCAGAGAGATGACCTGCGGAGACAAACCCGAGCTA 210
Qy 112 GTCCGAGAGACAGAGTGAACATTAAGATTTTACAAAGTCTCTCGTCTTCAAG 171
Db 211 GTCCGAGAGACAGAGTGAACATTAAGATTTTACAAAGTCTCTCGTCTTCAAG 270
Qy 172 GAGAAATGAGAGAACATTCAGTGTGGGAGAACTTCATGACATGAGTGTTCATGTC 231
Db 271 GAGAAATGAGAGAACATTCAGTGTGGGAGAACTTCATGACATGAGTGTTCATGTC 330
Qy 232 CTGAACCCGAGAGACAGAGTGGCAATGAGCTGTCCCTGACCTGCGGAGCTTCAAG 291
Db 331 CTGAACCCGAGAGACAGAGTGGCAATGAGCTGTCCCTGACCTGCGGAGCTTCAAG 390
Qy 292 GTCCGAGAGAACCTCTGTGTGCTGACCTTCCAGCTCCGAGAGCTCCGTCAGAG 351
Db 391 GTCCGAGAGAACCTCTGTGTGCTGACCTTCCAGCTCCGAGAGCTCCGTCAGAG 450
Qy 352 CTTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 411
Db 451 CTTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 510
Qy 412 GTCTACAGTTTATTTGATTTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 471
Db 511 GTCTACAGTTTATTTGATTTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 570
Qy 472 TTCAAACTGGGTGGGTGACAGGCTCTCTGACCTCGTGGGAGAGCTGTTCCTCAACA 531

Db 571 TTCAAACTGGGTGGGTGACAGGCTCTCTGACCTCGTGGGAGAGCTGTTCCTCAACA 630
Qy 532 GCCATCGACAGGTACATATTCATTTCAAGAGCCCTTGCCCTTAAAGATTTGTACAGG 591
Db 631 GCCATCGACAGGTACATATTCATTTCAAGAGCCCTTGCCCTTAAAGATTTGTACAGG 690
Qy 592 CCCAAGGCGGTGAGGCTTTTGGCTGATGTGACCAATAGCATTTGATGCGGTGCTG 651
Db 691 CCCAAGGCGGTGAGGCTTTTGGCTGATGTGACCAATAGCATTTGATGCGGTGCTG 750
Qy 652 CTTCTCTGAGGCTGAACTGCGAAGAACTGCATCTGTTTCTCAACATTTTCCACAC 711
Db 751 CTTCTCTGAGGCTGAACTGCGAAGAACTGCATCTGTTTCTCAACATTTTCCACAC 810
Qy 712 ATTGATGAACCTTACCTGATTTTGTGATGCGGCTTCAACGCTTCTGATTC 771
Db 811 ATTGATGAACCTTACCTGATTTTGTGATGCGGCTTCAACGCTTCTGATTC 870
Qy 772 GTGTATGCGTACATGTAATTTCTGGAAGGCTCAGAGCCAGCGCTCCGATGATTCAG 831
Db 871 GTGTATGCGTACATGTAATTTCTGGAAGGCTCAGAGCCAGCGCTCCGATGATTCAG 930
Qy 832 GTGCGACCCGAAAGACATCATTCACAGCTGTGAGATGGAAGTACAGGTACC 891
Db 931 GTGCGACCCGAAAGACATCATTCACAGCTGTGAGATGGAAGTACAGGTACC 990
Qy 892 CGGCGACCCGAAAGACATTCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 951
Db 991 CGGCGACCCGAAAGACATTCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1050
Qy 952 GTGTTGATCATCTGCTGGGCGCTCTGCTTCAATCATGATGATGATGATGATGATG 1011
Db 1051 GTGTTGATCATCTGCTGGGCGCTCTGCTTCAATCATGATGATGATGATGATGATG 1110
Qy 1012 ATGAACAAGCTCATTAAGACGTTGATGATGATGATGATGATGATGATGATGATG 1071
Db 1111 ATGAACAAGCTCATTAAGACGTTGATGATGATGATGATGATGATGATGATGATG 1170
Qy 1072 ACCGTGAACCCGATCATTCATGCTGAGAGTGAAGACCTGCGACACCTTCCGAGC 1131
Db 1171 ACCGTGAACCCGATCATTCATGCTGAGAGTGAAGACCTGCGACACCTTCCGAGC 1230
Qy 1132 ATGTTTCCCTTGTGAAGGACATGCGAGCTCTGTGTAACAGATGAGGAGACTCGAGC 1191
Db 1231 ATGTTTCCCTTGTGAAGGACATGCGAGCTCTGTGTAACAGATGAGGAGACTCGAGC 1290
Qy 1192 TGCCTGCAAAACAGCAACATGACAGCTGTTCAAGAGGCGCGAAGAGCTGCATC 1251
Db 1291 TGCCTGCAAAACAGCAACATGACAGCTGTTCAAGAGGCGCGAAGAGCTGCATC 1350
Qy 1252 AAGAGCAGGTCAAGATTGCCAAGGTAAACATGTCTGTCTCAGACAGACGTCTGCCGAG 1311
Db 1351 AAGAGCAGGTCAAGATTGCCAAGGTAAACATGTCTGTCTCAGACAGACGTCTGCCGAG 1410
Qy 1312 GCTCTGTGA 1320
Db 1411 GCTCTGTGA 1419

RESULT 5
US-10-225-567A-83
; Sequence 83, Application US/10225567A
; Publication No. US20030113798A1

; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144

PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 83
LENGTH: 1755
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-83

Query Match 95.3%; Score 1257.8; DB 6; Length 1755;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 52 ACTGACCTCTGGGAAAGTCCCTTCCAAAGAAAGATGACGCGGAGACAAACCCCGACGTA 111
DB 299 ACTTCTTTAGGGAGAGTCCCTTCCAAAGAAAGATGACGCGGAGACAAACCCCGACGTA 358
QY 112 GTCCGACGACCAAGGTGAACATTAAGAAATTTTACAAAGCTCTCTCTGCTTCAAG 171
DB 359 GTCCGACGACCAAGGTGAACATTAAGAAATTTTACAAAGCTCTCTCTGCTTCAAG 418
QY 172 GAGAAATGAGAGAAACATCCAGTGTGGGAGAACTTCATGACATAGAGTGTTCATGTC 231
DB 419 GAGAAATGAGAGAAACATCCAGTGTGGGAGAACTTCATGACATAGAGTGTTCATGTC 478
QY 232 CTGAACCCCGACGACGCTGGGCAATTGACATCTGCTGCTGACGCTGGGCACTTCCAG 291
DB 479 CTGAACCCCGACGACGCTGGGCAATTGACATCTGCTGCTGACGCTGGGCACTTCCAG 538
QY 292 GTCTGAGAGAACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 351
DB 539 GTCTGAGAGAACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 598
QY 352 CTTTCTTACCATTTATCGGACGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 411
DB 599 CTTTCTTACCATTTATCGGACGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 658
QY 412 GTCTGAGCTTATTTGATCTTCAACGCTGTTCACCGGAAAGATGACGCTGGGCTGGGCT 471
DB 659 GTCTGAGCTTATTTGATCTTCAACGCTGTTCACCGGAAAGATGACGCTGGGCTGGGCT 718
QY 472 TTCAAACTGGTGGGCTGACGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 531
DB 719 TTCAAACTGGTGGGCTGACGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 778
QY 532 GCCATGACAGGTACATATCCATTCAACAGGCCCCCTGGCTATPAAGAGATTGTCAACAG 591
DB 779 GCCATGACAGGTACATATCCATTCAACAGGCCCCCTGGCTATPAAGAGATTGTCAACAG 838
QY 592 CCCAAGGCGGTGGTGGCTGGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 651
DB 839 CCCAAGGCGGTGGTGGCTGGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 898
QY 652 CCTCTCTGGGCTGGAACCTGCAAGAACTGCAATCTGTTTGTCTGACAACTTTCCACAC 711
DB 899 CCTCTCTGGGCTGGAACCTGCAAGAACTGCAATCTGTTTGTCTGACAACTTTCCACAC 958
QY 712 ATTATGAACCTTACCTGATGTTCTGGAATCGGGGTCAACAGGCTACTGTTCTGTTCAATC 771
DB 959 ATTATGAACCTTACCTGATGTTCTGGAATCGGGGTCAACAGGCTACTGTTCTGTTCAATC 1018
QY 772 GTGTATGGTACATATATTTCTCTGGAAGGCTCAACGCAAGCCGTCGCAATGATTGAG 831
DB 1019 GTGTATGGTACATATATTTCTCTGGAAGGCTCAACGCAAGCCGTCGCAATGATTGAG 1078
QY 832 CGTGGACCCCAAGAGATCATTCACACAGTCTGAGATGGAGAGTACAGGTGAC 891
DB 1079 CGTGGACCCCAAGAGATCATTCACACAGTCTGAGATGGAGAGTACAGGTGAC 1138
QY 892 CGGCGACACCAAGCCCGCATGACATTAGGTTAGCCAAAGACCTGTGCTCTGATCTGCTG 951
DB 1139 CGGCGACACCAAGCCCGCATGACATTAGGTTAGCCAAAGACCTGTGCTCTGATCTGCTG 1198
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QY 952 GTGTATGATCTGCTGGGCGCTCTGCTGGAAATCAAGGTATGATCTTTGGAG 1011
DB 1199 GTGTATGATCTGCTGGGCGCTCTGCTGGAAATCAAGGTATGATCTTTGGAG 1258
QY 1012 ATGAACAGCTCATTTAAGACGGTGTGTTGCAATCTGACAGTATCTGCTGCTGAACTCC 1071
DB 1259 ATGAACAGCTCATTTAAGACGGTGTGTTGCAATCTGACAGTATCTGCTGCTGAACTCC 1318
QY 1072 ACCGTGAACCCCATCATCTATGCTCTGAGAGTAAGACCTGCAACGCTTCCGAGC 1131
DB 1319 ACCGTGAACCCCATCATCTATGCTCTGAGAGTAAGACCTGCAACGCTTCCGAGC 1378
QY 1132 ATGTTTCCCTCTTGGAGGCACTGCGAGCCTCTGATTAACAGATGGGGACCTCGAC 1191
DB 1379 ATGTTTCCCTCTTGGAGGCACTGCGAGCCTCTGATTAACAGATGGGGACCTCGAC 1438
QY 1192 TCCCTGCAAAACAGCAACATGACAGCTGTTCAAGGGCCGCAAAAGCTGCAATC 1251
DB 1439 TCCCTGCAAAACAGCAACATGACAGCTGTTCAAGGGCCGCAAAAGCTGCAATC 1498
QY 1252 AAGACAGGCTCAAGATTGCCAAGGTAAACATGCTGTGTCCACAGACACGCTGCGAG 1311
DB 1499 AAGACAGGCTCAAGATTGCCAAGGTAAACATGCTGTGTCCACAGACACGCTGCGAG 1558
QY 1312 GCTCTGTGA 1320
DB 1559 GCTCTGTGA 1567
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RESULT 6
US-10-295-027-235
Sequence 235, Application US/10295027
Publication No. US2003023250A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevez, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 235

LENGTH: 1755
TYPE: DNA
ORGANISM: Homo sapiens
US-10-295-027-235

Query Match 95.3%; Score 1257.8; DB 7; Length 1755;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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OY 52 ACTGACCTCTGGGAAGTCCCTTCCAGAGAAAGATGATCTGCGGGAGACACCCCACTA 111
DB 299 ACTTCCTTTAGGGGAAGTCCCTTCCAGAGAAAGATGATCTGCGGGAGACACCCCACTA 358
OY 112 GTCCAGAGACCAAGTGAACATTAAGAAATTTTCAACAAGTCTCTCGGCTTCAAG 171
DB 359 GTCCAGAGACCAAGTGAACATTAAGAAATTTTCAACAAGTCTCTCGGCTTCAAG 418
OY 172 GAGAAATGAGAGAACATCAAGTGTGGGGAGAACTTCAATGACATAGAGTGTTCATGATC 231
DB 419 GAGAAATGAGAGAACATCAAGTGTGGGGAGAACTTCAATGACATAGAGTGTTCATGATC 478
OY 232 CTGAACCCCAAGCAGACAGTGGCCATTGCAATCTCTGTCTTCAAGCTGGGACCTTCAAG 291
DB 479 CTGAACCCCAAGCAGACAGTGGCCATTGCAATCTCTGTCTTCAAGCTGGGACCTTCAAG 538
OY 292 GTCCAGAGAACCTCTGGTGTGTCGCTCATCTCCAGAGCCTCGGCTGCAAG 351
DB 539 GTCCAGAGAACCTCTGGTGTGTCGCTCATCTCCAGAGCCTCGGCTGCAAG 598
OY 352 CTTCTCTACCACTTCAATGCGCAGCCTGGCGGTGGAGAACCTCTGGGGAGTGTCAATTTT 411
DB 599 CTTCTCTACCACTTCAATGCGCAGCCTGGCGGTGGAGAACCTCTGGGGAGTGTCAATTTT 658
OY 412 GTCTACAGCTTATATGATCTTCCAGAGTGTTCACCGGAAAGATAGCCGCAAGTGTTCG 471
DB 659 GTCTACAGCTTATATGATCTTCCAGAGTGTTCACCGGAAAGATAGCCGCAAGTGTTCG 718
OY 472 TTCAAACTGGGTGGGTGTCAGCGGCTCTTCACTGCGCTCGGTGGGAGAGCTGTTCCTACA 531
DB 719 TTCAAACTGGGTGGGTGTCAGCGGCTCTTCACTGCGCTCGGTGGGAGAGCTGTTCCTACA 778
OY 532 GCCATGCAAGGTATCATATTCATTCAACAGGCCCTTGCCCTATAGAGATGTGTCACAG 591
DB 779 GCCATGCAAGGTATCATATTCATTCAACAGGCCCTTGCCCTATAGAGATGTGTCACAG 838
OY 592 CCCAAGGCCGTGTAGCGTTTGGCTGATGTGACCATATGCAATGTGTGCGCGTGTG 651
DB 839 CCCAAGGCCGTGTAGCGTTTGGCTGATGTGACCATATGCAATGTGTGCGCGTGTG 898
OY 652 CCTCTCTGGGCTGGAACCTGCGAAGAACTGCAATCTGTTGCTCAGACATTTTCCACAG 711
DB 899 CCTCTCTGGGCTGGAACCTGCGAAGAACTGCAATCTGTTGCTCAGACATTTTCCACAG 958
OY 712 ATTGATGAACCTTACCTGATGTGTGATCGGGGTGACCAAGGATACGTGTTCTGTTCATC 771
DB 959 ATTGATGAACCTTACCTGATGTGTGATCGGGGTGACCAAGGATACGTGTTCTGTTCATC 1018
OY 772 GTGTATGCGTATATGTATTTCTTGGAAAGGCTCACAGCAGCCGCTCGGATGATTCAG 831
DB 1019 GTGTATGCGTATATGTATTTCTTGGAAAGGCTCACAGCAGCCGCTCGGATGATTCAG 1078
OY 832 CGTGCACCCAGAGAGCATCATCACTCAAGTCTGAGAGTGGGAGGTAAGGTGAC 891
DB 1079 CGTGCACCCAGAGAGCATCATCACTCAAGTCTGAGAGTGGGAGGTAAGGTGAC 1138
OY 892 CGGCGAGACCAAGCCCGCATGACATTAAGTTAGCCAAAGCCCTGTCTCTGATCTGTG 951
DB 1139 CGGCGAGACCAAGCCCGCATGACATTAAGTTAGCCAAAGCCCTGTCTCTGATCTGTG 1198
OY 952 GTGTGATCATCTGTGGGGCCCTGTGCTTGGAAATCATAGGTATGATCTTTGGGAAG 1011
DB 1199 GTGTGATCATCTGTGGGGCCCTGTGCTTGGAAATCATAGGTATGATCTTTGGGAAG 1258
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OY 1012 ATGAACAAGCTCATTAAGACGGTGTTCATTTCTGACAGTATGCTCTGCTGTGAACCTCC 1071
DB 1259 ATGAACAAGCTCATTAAGACGGTGTTCATTTCTGACAGTATGCTCTGCTGTGAACCTCC 1318
OY 1072 ACCGTGAACCCCATCATCTATGCTCTGAGAGTAAGACCTGCAACAGCTTTCGGAGC 1131
DB 1319 ACCGTGAACCCCATCATCTATGCTCTGAGAGTAAGACCTGCAACAGCTTTCGGAGC 1378
OY 1132 ATGTTTCCCTTTTGTGAAGGACATGCGAGCTCTGTGATTAACAATAGGGGAGCTGGAC 1191
DB 1379 ATGTTTCCCTTTTGTGAAGGACATGCGAGCTCTGTGATTAACAATAGGGGAGCTGGAC 1438
OY 1192 TGCCGTGACAAACACGCAAAACATGACACAGTGTTCACAGGGCGGAGAAAGCTGCATC 1251
DB 1439 TGCCGTGACAAACACGCAAAACATGACACAGTGTTCACAGGGCGGAGAAAGCTGCATC 1498
OY 1252 AAGAGCAGGTCAAGATTTGCCAAGTAAACATGTCTGTGTCCACAGACAGTCTGCGAG 1311
DB 1499 AAGAGCAGGTCAAGATTTGCCAAGTAAACATGTCTGTGTCCACAGACAGTCTGCGAG 1558
OY 1312 GCTCTGTA 1320
DB 1559 GCTCTGTA 1567
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RESULT 7

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US-11-127-877-2
; Sequence 2, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitael, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127, 877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-2
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Query Match 95.3%; Score 1257.8; DB 15; Length 1755;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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OY 52 ACTGACCTCTGGGAAGTCCCTTCCAGAGAAAGATGATCTGCGGGAGACACCCCACTA 111
DB 299 ACTTCCTTTAGGGGAAGTCCCTTCCAGAGAAAGATGATCTGCGGGAGACACCCCACTA 358
OY 112 GTCCAGAGACCAAGTGAACATTAAGAAATTTTCAACAAGTCTCTCGTCTTCAAG 171
DB 359 GTCCAGAGACCAAGTGAACATTAAGAAATTTTCAACAAGTCTCTCGTCTTCAAG 418
OY 172 GAGAAATGAGAGAACATCAAGTGTGGGGAGAACTTCAATGACATAGAGTGTTCATGATC 231
DB 419 GAGAAATGAGAGAACATCAAGTGTGGGGAGAACTTCAATGACATAGAGTGTTCATGATC 478
OY 232 CTGAACCCCAAGCAGACAGTGGCCATTGCAATCTCTGTCTTCAAGCTGGGACCTTCAAG 291
DB 479 CTGAACCCCAAGCAGACAGTGGCCATTGCAATCTCTGTCTTCAAGCTGGGACCTTCAAG 538
OY 292 GTCTGAGAAACCTCTGGTGTGTCGCTCATCTCCAGAGCCTCGGCTGCAAG 351
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Db	539	GTCTCTGAGAACTCTGGTGGTGGTGCATCTCTCACTCCGGCAGGCTCCGGCTCAAG	58
QY	352	CCTTCTTACCACTTATCGGCAAGCTCGGGGTGGCAAGACTCTG393AGGTGCATTTT	411
Db	599	CTTCTCTACACTTCAATCGGCAAGCTCGGGGTGGCAAGACTCTG393AGGTGCATTTT	658
QY	412	GTCTCAGCTTATGATCTTCAAGGTTCACAGGAAAGATGACCGCAACGTGTTTCG	471
Db	659	GTCTCAGCTTATGATCTTCAAGGTTCACAGGAAAGATGACCGCAACGTGTTTCG	718
QY	472	TTCAAACTGGGTGGGTCAAGGCTCTCTTCACTGCGTCCGGTGGGAGGCTGTCTCA	531
Db	719	TTCAAACTGGGTGGGTCAAGGCTCTCTTCACTGCGTCCGGTGGGAGGCTGTCTCA	778
QY	532	GCATTCGACAGGTACATTCATTCACAGGCCCCTG3CTTAATAAGATTTGCACAG	591
Db	779	GCATTCGACAGGTACATTCATTCACAGGCCCCTG3CTTAATAAGATTTGCACAG	838
QY	592	CCCAAGCCGTGGTACGCTTTTGGCTGAATGGACATAGCCATTGTGATCGCCGTG	651
Db	839	CCCAAGCCGTGGTACGCTTTTGGCTGAATGGACATAGCCATTGTGATCGCCGTG	898
QY	652	CCTCTCTGGGCTGGAACCTCGGAGAACTGCAATCTGTTTGCTCAACAATTTCCACAC	711
Db	899	CCTCTCTGGGCTGGAACCTCGGAGAACTGCAATCTGTTTGCTCAACAATTTCCACAC	958
QY	712	ATTGATGAACCTACCTGATGTTCGTGATCGGGGTCAAGAGCTGCTGTCTGTATC	771
Db	959	ATTGATGAACCTACCTGATGTTCGTGATCGGGGTCAAGAGCTGCTGTCTGTATC	1011
QY	772	GTGTATGCGTACATGTATATTCTTGGAAAGGCTCACAGCCAGCGCTCGCATATTCA	831
Db	1019	GTGTATGCGTACATGTATATTCTTGGAAAGGCTCACAGCCAGCGCTCGCATATTCA	1077
QY	832	CGTGGCAACCCAGAAAGCATCATATCCAAGCTGAGAGATGGAAAGTACAGGTAC	891
Db	1079	CGTGGCAACCCAGAAAGCATCATATCCAAGCTGAGAGATGGAAAGTACAGGTAC	1133
QY	892	CGGCGAGACCAAGCCCGCATGAGCATTAAGTTAGCCAAACCCTGTCTCTGATCTG3TG	951
Db	1139	CGGCGAGACCAAGCCCGCATGAGCATTAAGTTAGCCAAACCCTGTCTCTGATCTG3TG	1199
QY	952	GTGTGATCATCTGCTGGGGCCCTGTGCTTGCAATCATG3GTGATGATCTTTGGGA	1011
Db	1199	GTGTGATCATCTGCTGGGGCCCTGTGCTTGCAATCATG3GTGATGATCTTTGGGA	1251
QY	1012	ATGAACAAGCTATTAAAGCGGTTTGAATTCGAGATATGCTCTGCTCTGAACTCC	107
Db	1259	ATGAACAAGCTATTAAAGCGGTTTGAATTCGAGATATGCTCTGCTCTGAACTCC	1311
QY	1072	ACCGTGAACCCCATCATCTATGCTCTGAAGAGTAAAGGACCTGCGACACGCTTTCGAGAC	113
Db	1319	ACCGTGAACCCCATCATCTATGCTCTGAAGAGTAAAGGACCTGCGACACGCTTTCGAGAC	1377
QY	1132	ATGTTTCCCTCTTGTGAAGGCACTGGGACGCTCTGGAATAACGATGGGGGCTCGAGC	1433
Db	1439	ATGTTTCCCTCTTGTGAAGGCACTGGGACGCTCTGGAATAACGATGGGGGCTCGAGC	1499
QY	1439	TGCTTCGACAAACAGCGAAACATGACGCAATGTTCACAGGGCCGCAAAAAGCTGCATC	1499
Db	1499	TGCTTCGACAAACAGCGAAACATGACGCAATGTTCACAGGGCCGCAAAAAGCTGCATC	1555
QY	1312	GCTCTGTGA 1320	
Db	1559	GCTCTGTGA 1567	

	/ Sequence 27, Application US/11019829	
	/ Publication No. US20050136465A1	
	/ GENERAL INFORMATION:	
	/ APPLICANT: Hoffmann-La Roche Inc.	
	/ TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat	
	/ FILE REFERENCE: 22304	
	/ CURRENT APPLICATION NUMBER: US/11/019,829	
	/ CURRENT FILING DATE: 2004-12-22	
	/ NUMBER OF SEQ ID NOS: 146	
	/ SOFTWARE: PatentIn version 3.2	
	/ SEQ ID NO 27	
	/ LENGTH: 5480	
	/ TYPE: DNA	
	/ ORGANISM: Homo sapiens	
	/ FEATURE:	
	/ NAME/KEY: cannabinoid receptor 1 (brain) variant 1	
	/ LOCATION: (1)..(5480)	
	/ OTHER INFORMATION: LocusID: 1268; NM_016083	
	US-11-019-829-27	
	Query Match	95.3%; Score 1257, 8; DB 13; Length 5480;
	Best Local Similarity	99.4%; Pred. No. 0;
	Matches 1262; Conservative	0; Mismatches 7; Indels 0; Gaps 0
QY	52 ACTGACCTTCGTGGGAAGTCCCTTCACAAGAAGATGACTCGGGAGAACCCCCAGCTTA	111
DB	214 ACTTCCTTTAAGGGGAAGTCCCTTCACAAGAAGATGACTCGGGAGAACCCCCAGCTTA	273
QY	112 GTCCAGAGACCGAGTGAACTTACAGAAATTTCACAAAGTCTCTCCGCTCCTCAAG	171
DB	274 GTCCAGAGACCGAGTGAACTTACAGAAATTTCACAAAGTCTCTCCGCTCCTCAAG	333
QY	172 GAGATGAGAGAAACATCATCGTGTGGGAGAACTTCATGACATAGAGTTCATGATC	231
DB	334 GAGATGAGAGAAACATCATCGTGTGGGAGAACTTCATGACATAGAGTTCATGATC	393
QY	232 CTGAACCCCAAGCAGACGTGCGCATTCAGATCTGTCCTTCACGCTGCGCACCTTCACG	291
DB	394 CTGAACCCCAAGCAGACGTGCGCATTCAGATCTGTCCTTCACGCTGCGCACCTTCACG	453
QY	292 GTCCGTGAGAACTCTCTGT	351
DB	454 GTCCGTGAGAACTCTCTGT	513
QY	352 CCTTCCTACCACTTCATCGGAGCCTGCGGAGTGCAGACCTTCCTGGGAGTGTCAATTTT	411
DB	514 CCTTCCTACCACTTCATCGGAGCCTGCGGAGTGCAGACCTTCCTGGGAGTGTCAATTTT	573
QY	412 GTCTACAGCTTCATTCAGTTCACAGTGTTCACACCGCAAGATAGCCGCAACGTGTTCG	471
DB	574 GTCTACAGCTTCATTCAGTTCACAGTGTTCACACCGCAAGATAGCCGCAACGTGTTCG	633
QY	472 TTCAAACGTGGGTGGGTGACGGGCTCTTCACCTGCTCCGTGGGAGAGCTGTTCCTACA	531
DB	634 TTCAAACGTGGGTGGGTGACGGGCTCTTCACCTGCTCCGTGGGAGAGCTGTTCCTACA	693
QY	532 GCATTCGACAGATTCATATTCATTCACAGGCCCGGCTCTTAAGAGATTTGTACACAGG	591
DB	694 GCATTCGACAGATTCATATTCATTCACAGGCCCGGCTCTTAAGAGATTTGTACACAGG	753
QY	592 CCCAAGGCGGTGTAGCGTTTTGTGCTGATGTGACCATAGGCATTTGATGCGCGGTGCTG	651
DB	754 CCCAAGGCGGTGTAGCGTTTTGTGCTGATGTGACCATAGGCATTTGATGCGCGGTGCTG	813
QY	652 CCTCTCTGGGCTGGAACCTGCGAAGAACTGCAATCTGTTTGTCTCAGACATTTTCCCACAC	711
DB	814 CCTCTCTGGGCTGGAACCTGCGAAGAACTGCAATCTGTTTGTCTCAGACATTTTCCCACAC	873
QY	712 ATTGATGAAAACCTACCTGATGTTGTCGATCGGGGTACCAAGGTATCTGCTTCTGTTATC	771
DB	874 ATTGATGAAAACCTACCTGATGTTTCTGATCGGGGTACCAAGGTATCTGCTTCTGTTATC	933
QY	772 GTGATGCGTACATGATATCTCTGGAAGGCTCACAGCCAGCGCGTCCGATGATTCAG	831

Db 924 GTGATGGGTACATGATTAATTTCTTGGAAGCTCAAGCAGCCGTCGATGATTCAG 993
Qy 832 CGTGACCCCAAGAAAGCATCATCTCAACAGCTCTGAGAGATGGAGATCAAGGTGAC 891
Db 994 CGTGACCCCAAGAAAGCATCATCTCAACAGCTCTGAGAGATGGAGATCAAGGTGAC 1053
Qy 892 CGGCGACCAAGCCCGCATGAGCATTAAGGTTAGCCAGAACCTGTGCTGATCCGTG 951
Db 1054 CGGCGACCAAGCCCGCATGAGCATTAAGGTTAGCCAGAACCTGTGCTGATCCGTG 1113
Qy 952 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGCTGATGATGCTTTGGGAG 1011
Db 1114 GTGTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGCTGATGATGCTTTGGGAG 1173
Qy 1012 ATGAACAAGCTATTAAAGCGGTGTTTGATTTCTGAGATAGTCTGCTGCTGAATCC 1071
Db 1174 ATGAACAAGCTATTAAAGCGGTGTTTGATTTCTGAGATAGTCTGCTGCTGAATCC 1233
Qy 1072 ACCGTGAACCCCATCATATGCTCTGAGAGATGAAGAACCTGCGACAGCTTTCGGAGC 1131
Db 1234 ACCGTGAACCCCATCATATGCTCTGAGAGATGAAGAACCTGCGACAGCTTTCGGAGC 1293
Qy 1132 ATGTTTCCCTCTTGTGAAGGCACTGGCAGCCTCTGATTAACAGCATGGGGGACTCGAC 1191
Db 1294 ATGTTTCCCTCTTGTGAAGGCACTGGCAGCCTCTGATTAACAGCATGGGGGACTCGAC 1353
Qy 1192 TGCCGTGCAAAACGCAAAACATGACGACATGTTTCAAGGGCCGCAAAAGCTGCAATC 1251
Db 1354 TGCCGTGCAAAACGCAAAACATGACGACATGTTTCAAGGGCCGCAAAAGCTGCAATC 1413
Qy 1252 AAGAGACGGTCAAGATTGCGAAGGTGACATGTCGTGTCACAGACAGCTCTGCCGAG 1311
Db 1414 AAGAGACGGTCAAGATTGCGAAGGTGACATGTCGTGTCACAGACAGCTCTGCCGAG 1473
Qy 1312 GCTCTGTGA 1320
Db 1474 GCTCTGTGA 1482

RESULT 9
US-10-208-408-52
; Sequence 52, Application US/10208408
; Publication No. US20030096272A1
; GENERAL INFORMATION:
; APPLICANT: Scheye, Xiao Min
; TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
; FILE REFERENCE: PA-0048-1 US
; CURRENT APPLICATION NUMBER: US/10/208,408
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,868
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 52
; LENGTH: 5653
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030096272A1 1383759.1
US-10-208-408-52

Query Match 95.3%; Score 1257.8; DB 6; Length 5653;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1862; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 52 ACTGACCTCTGGAAGTCCCTTCAAGAGAGATGACGCGGAGACAAACCCCAAGCTA 111
Db 260 ACTTCTTTAAGGGAAGTCCCTTCAAGAGAGATGACGCGGAGACAAACCCCAAGCTA 319
Qy 112 GTCCGACAGACGAGGTGAACATTACAGATTTTACAAAGTCTCTGTCCTTCAAG 171

Db 320 GTCCGACAGACGAGTGAACATTACAGAAATTTTACAAAGTCTCTGTCCTTCAAG 379
Qy 172 GAGAAATGAGAGAAATCATCAGTGTGGGAGAACTTCAATGACATAGAGTGTTCAGTGC 231
Db 380 GAGAAATGAGAGAAATCATCAGTGTGGGAGAACTTCAATGACATAGAGTGTTCAGTGC 439
Qy 232 CTGAACCCCAAGCCAGACAGCTGGCATTTGCACTCTGTCCTTCAAGCTGGGACCTTCAAG 291
Db 440 CTGAACCCCAAGCCAGACAGCTGGCATTTGCACTCTGTCCTTCAAGCTGGGACCTTCAAG 499
Qy 292 GTCTGAGAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 351
Db 500 GTCTGAGAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 559
Qy 352 CTTTCTTACCACTTCACTGAGAGCTGGCGGTGGGAGACCTCTGCGGAGTGTATTTT 411
Db 560 CTTTCTTACCACTTCACTGAGAGCTGGCGGTGGGAGACCTCTGCGGAGTGTATTTT 619
Qy 412 GTCTACAGCTTCAATTAATTTCAAGTGTTCACAGCCGACCAAGATAGCCGCAAGTGTTCG 471
Db 620 GTCTACAGCTTCAATTAATTTCAAGTGTTCACAGCCGACCAAGATAGCCGCAAGTGTTCG 679
Qy 472 TTCAAACTGGGTGGGTGACAGGCTCTTCACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCA 531
Db 680 TTCAAACTGGGTGGGTGACAGGCTCTTCACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCA 739
Qy 532 GCAATCGACAGTTCATATTCATTTCAAGGCTGGGCTTAAAGAGATTTGTCACAGG 591
Db 740 GCAATCGACAGTTCATATTCATTTCAAGGCTGGGCTTAAAGAGATTTGTCACAGG 799
Qy 592 CCCAAGGCGGTGTAAGCTGTTTGTGCTGATGTAACATAGCAATTTGATGCGGTGCTG 651
Db 800 CCCAAGGCGGTGTAAGCTGTTTGTGCTGATGTAACATAGCAATTTGATGCGGTGCTG 859
Qy 652 CCTCTCTGCGCTGGAATCTGGAAGAACTGCAATCTGTTTCTCAAGACATTTTCCACAC 711
Db 860 CCTCTCTGCGCTGGAATCTGGAAGAACTGCAATCTGTTTCTCAAGACATTTTCCACAC 919
Qy 712 ATGATGAACCTTACCTGATGTTCTGAGATGGGGGACACAGAGTACCTGCTGTCATC 771
Db 920 ATGATGAACCTTACCTGATGTTCTGAGATGGGGGACACAGAGTACCTGCTGTCATC 979
Qy 772 GTGTGCGTACATGATATTTCTCTGGAAGGCTCAAGCCAGCGCTGCGATGATTCAG 831
Db 980 GTGTGCGTACATGATATTTCTCTGGAAGGCTCAAGCCAGCGCTGCGATGATTCAG 1039
Qy 832 CGTGACCCCAAGAAAGCATCATCTCAACAGCTCTGAGATGGAGATGGAGATCAAGGTGAC 891
Db 1040 CGTGACCCCAAGAAAGCATCATCTCAACAGCTCTGAGATGGAGATGGAGATCAAGGTGAC 1099
Qy 892 CGGCGACCAAGCCCGCATGAGCATTAAGGTTAGCCAGAACCTGTGCTGATCCGTG 951
Db 1100 CGGCGACCAAGCCCGCATGAGCATTAAGGTTAGCCAGAACCTGTGCTGATCCGTG 1159
Qy 952 GTGTGATCATCTGCTGGGGCCCTCTGCTTCAATCATGCTGATGATGCTTTGGGAG 1011
Db 1160 GTGTGATCATCTGCTGGGGCCCTCTGCTTCAATCATGCTGATGATGCTTTGGGAG 1219
Qy 1012 ATGAACAAGCTATTAAAGCGGTGTTTGATTTCTGAGATAGTCTGCTGCTGAATCC 1071
Db 1220 ATGAACAAGCTATTAAAGCGGTGTTTGATTTCTGAGATAGTCTGCTGCTGAATCC 1279
Qy 1072 ACCGTGAACCCCATCATATGCTCTGAGAGATGAAGAACCTGCGACAGCTTTCGGAGC 1131
Db 1280 ACCGTGAACCCCATCATATGCTCTGAGAGATGAAGAACCTGCGACAGCTTTCGGAGC 1339
Qy 1132 ATGTTTCCCTCTTGTGAAGGCACTGGCAGCCTCTGATTAACAGATGGGGGACTCGAC 1191
Db 1340 ATGTTTCCCTCTTGTGAAGGCACTGGCAGCCTCTGATTAACAGATGGGGGACTCGAC 1399
Qy 1192 TGCCGTGCAAAACGCAAAACATGACGACATGTTTCAAGGGCCGCAAAAGCTGCAATC 1251
Db 1400 TGCCGTGCAAAACGCAAAACATGACGACATGTTTCAAGGGCCGCAAAAGCTGCAATC 1459

Query Match	95.2%	Score 1256.2	DB 10	Length 1419
Best Local Similarity	99.4%	Pred. No. 0		
Matches 1261	Conservative 0	Mismatches 8	Indels 0	Gaps 0

Dd		691	CCCAAGCGCTGCTGGCGTTTGCTGTATGTGAACCATTCGCATTGTGATTCGCCGTGCTG	750
Oy		652	CCTCTCCTGGGTGAGAACCTGCGAAGAACTGCAATCTGTTTGGTCAACAATTTTCCACAC	711
Dd		751	CCTCTCCTGGGTGAGAACCTGCGAAGAACTGCAATCTGTTTGGTCAACAATTTTCCACAC	810
Oy		712	ATTGATGAAACCTTAACCTGATGTTCTTGATCGGGGTGACCAAGGTACTGCTTGTGTCATC	771
Dd		811	ATTGATGAAACCTTAACCTGATGTTCTTGATCGGGGTGACCAAGGTACTGCTTGTGTCATC	870
Oy		772	GNGATGAGTACATGATATATTTCTTGGAAGGCTCACAGCCAGCCGTCGGANTGATTCAG	831
Dd		871	GNGATGAGTACATGATATATTTCTTGGAAGGCTCACAGCCAGCCGTCGGANTGATTCAG	930
Oy		832	CGTGACACCAGAAGAGCATCATCCACACGTCGAGATGGGAAGGTACAGGTGACC	891
Dd		931	CGTGACACCAGAAGAGCATCATCCACACGTCGAGATGGGAAGGTACAGGTGACC	990
Oy		892	CGGCCAAGCCAAAGCCCGCATGAGCATTTAGGTTTAGCCAAAGCCCTGGTCTGATCCTGGTG	951
Dd		991	CGGCCAAGCCAAAGCCCGCATGAGCATTTAGGTTTAGCCAAAGCCCTGGTCTGATCCTGGTG	1050
Oy		952	GTGTTGATCATCTGTGCGGGCCCTGCTTGCAATCAAGTGATGATGTTCTTTGGGAAG	1011
Dd		1051	GTGTTGATCATCTGTGCGGGCCCTGCTTGCAATCAAGTGATGATGTTCTTTGGGAAG	1110
Oy		1012	ATGAACAAGCTCATTTAAGACGGTGTGTTGCATTTCTGACATGTCCTGCTGCTGAACCTCC	1071
Dd		1111	ATGAACAAGCTCATTTAAGACGGTGTGTTGCATTTCTGACATGTCCTGCTGCTGAACCTCC	1170
Oy		1072	ACCGTGAACCCCATCATCTATGCTCTGAGAGTAAGACCTGCGACACGCTTTCCGGAGC	1131
Dd		1171	ACCGTGAACCCCATCATCTATGCTCTGAGAGTAAGACCTGCGACACGCTTTCCGGAGC	1230
Oy		1132	ATGTTTCCCTTTTGAAGGACCTGCGAGCCTCTGAGTAACAGATGGGGACCTCGGAC	1191
Dd		1231	ATGTTTCCCTTTTGAAGGACCTGCGAGCCTCTGAGTAACAGATGGGGACCTCGGAC	1290
Oy		1192	TGCTGCAACAACACGCAAAACATGACAGCCAGTGTTCACAGGGCCGCGAAGAGCTGCATC	1251
Dd		1291	TGCTGCAACAACACGCAAAACATGACAGCCAGTGTTCACAGGGCCGCGAAGAGCTGCATC	1350
Oy		1252	AAGAGCAGGTCAAGATTGCCAAGGTAAACAATGTCGTGTCCAAGACACGTCCTGCGAG	1311
Dd		1351	AAGAGCAGGTCAAGATTGCCAAGGTAAACAATGTCGTGTCCAAGACACGTCCTGCGAG	1410
Oy		1312	GCTCTGTGA 1320	
Dd		1411	GCTCTGTGA 1419	
RESULT 11				
US-10-521-420-3				
Sequence 3, Application US/10521420				
GENERAL INFORMATION:				
APPLICANT: Greasley, Peter				
TITLE OF INVENTION: Methods to Identify True Antagonists and Inverse Agonists of the				
FILE REFERENCE: ASD-P01-752				
CURRENT APPLICATION NUMBER: US/10/521,420				
PRIORITY FILING DATE: 2005-01-14				
PRIOR FILING DATE: 2002-07-17				
NUMBER OF SEQ ID NOS: 4				
SOFTWARE: PatentIn Ver. 2.1				
SEQ ID NO 3				
LENGTH: 1419				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-10-521-420-3				
Query Match				
95.2%; Score 1256.2; DB 10; Length 1419;				

Best Local Similarity 99.4%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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OY 52 ACTGACCTTCGGGAAGTCCCTTCCAGAGAAAGATGCTGCGGGAGACACCCCGAGCTA 111
Db 151 ACTTCCTTAGGGGAAGTCCCTTCCAGAGAAAGATGCTGCGGGAGACACCCCGAGCTA 210
OY 112 GTCCAGAGACACAGGTGAACATTAAGAAATTTTCAACAAGTCTCTCGCTCCCTCAAG 171
Db 211 GTCCAGAGACACAGGTGAACATTAAGAAATTTTCAACAAGTCTCTCGCTCCCTCAAG 270
OY 172 GAGAAATGAGAGAAATCATCCAGTGTGGGAGAACTTTCATGAGACATAGAGTGTTCATGTC 231
Db 271 GAGAAATGAGAGAAATCATCCAGTGTGGGAGAACTTTCATGAGACATAGAGTGTTCATGTC 330
OY 232 CTGAACCCCGACGACAGCTGGCCATTTGCAATGCTCTGCTCCCTCAAGCTGGGACCTTCAAG 291
Db 331 CTGAACCCCGACGACAGCTGGCCATTTGCAATGCTCTGCTCCCTCAAGCTGGGACCTTCAAG 390
OY 292 GTCCGAGAAACCTCTGGTGTGCGGTCACTCCACTCCGAGAGCTCCGCTGCAAG 351
Db 391 GTCCGAGAAACCTCTGGTGTGCGGTCACTCCACTCCGAGAGCTCCGCTGCAAG 450
OY 352 CCTTCCTACCACTTCATCGGCAAGCTGGCGGTGGAGACCTTCGAGAGTGTCAATTTT 411
Db 451 CCTTCCTACCACTTCATCGGCAAGCTGGCGGTGGAGACCTTCGAGAGTGTCAATTTT 510
OY 412 GTCTACAGCTTCATTTGACTTCCAGCTGTTCCACCGCAAAATAGACCGCACTGTTCTG 471
Db 511 GTCTACAGCTTCATTTGACTTCCAGCTGTTCCACCGCAAAATAGACCGCACTGTTCTG 570
OY 472 TTCAAACTGGGTGGGGGTCAAGGCTCTTCACTGCGCTCGGGAGAGCTGTTCTTCA 531
Db 571 TTCAAACTGGGTGGGGGTCAAGGCTCTTCACTGCGCTCGGGAGAGCTGTTCTTCA 630
OY 532 GCCATGACAGGTACATATCCATTGACAGAGCCCTGAGCTATTAAGAGATTTGTCAAG 591
Db 631 GCCATGACAGGTACATATCCATTGACAGAGCCCTGAGCTATTAAGAGATTTGTCAAG 690
OY 592 CCCAAGGCCGTGTAGCGTTTGGCTGATGTGAACATATGCAATTTGATGCGCTGCTG 651
Db 691 CCCAAGGCCGTGTAGCGTTTGGCTGATGTGAACATATGCAATTTGATGCGCTGCTG 750
OY 652 CCTCTCTGGGCTGGAACCTGAGAAACCTGAATCTGTTGCTCAGACATTTTCCCAAC 711
Db 751 CCTCTCTGGGCTGGAACCTGAGAAACCTGAATCTGTTGCTCAGACATTTTCCCAAC 810
OY 712 ATTGATGAACCTTACCTGATGTTCTGGAATCGGGGTCAACAGCGTACTGCTTCTGTCATC 771
Db 811 ATTGATGAACCTTACCTGATGTTCTGGAATCGGGGTCAACAGCGTACTGCTTCTGTCATC 870
OY 772 GTGTATGGGTACATGTATTTCTCTGGAAGGCTCAAGCAAGCCGCTCGGATGATTCAG 831
Db 871 GTGTATGGGTACATGTATTTCTCTGGAAGGCTCAAGCAAGCCGCTCGGATGATTCAG 930
OY 832 CGTGGACCCCAAGAGACATCATCCAGAGCTCTGAGAGTGGAGAGTACAGGTGACC 891
Db 931 CGTGGACCCCAAGAGACATCATCCAGAGCTCTGAGAGTGGAGAGTACAGGTGACC 990
OY 892 CGGCGACAGCAAGCCCGCATGACATTAAGTTAGCCAAAGCCCTGCTCTGATCTGCTG 951
Db 991 CGGCGACAGCAAGCCCGCATGACATTAAGTTAGCCAAAGCCCTGCTCTGATCTGCTG 1050
OY 952 GTGTGATGATCTGTCTGGGGCCCTGCTGCTTGCATATATGTGTATGATCTTTTGGAG 1011
Db 1051 GTGTGATGATCTGTCTGGGGCCCTGCTGCTTGCATATATGTGTATGATCTTTTGGAG 1110
OY 1012 ATGAACAAGCTCATTAAGAAGGTTTGAATCTGAGATATGCTGCGCTGCGAATCTC 1071
Db 1111 ATGAACAAGCTCATTAAGAAGGTTTGAATCTGAGATATGCTGCGCTGCGAATCTC 1170
OY 1072 ACCGTGAACCCCATCATCTATGCTCTGAGAGATTAAGACCTGCGACACGCTTTCGGAGC 1131
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Db 1171 ACCGTGAACCCCATCATCTATGCTCTGAGAGATTAAGACCTGCGACACGCTTTCGGAGC 1230
OY 1132 ATGTTCCCTCTGTGGAAGGACATGCGAGCTCTGGAATTAACATATGGGGAGCTCGGAC 1191
Db 1231 ATGTTCCCTCTGTGGAAGGACATGCGAGCTCTGGAATTAACATATGGGGAGCTCGGAC 1290
OY 1192 TGCCGTGCAAAACACGCAAAACAATGACACAGTGTTCACAGGGCGGAGAAAGCTGCATC 1251
Db 1291 TGCCGTGCAAAACACGCAAAACAATGACACAGTGTTCACAGGGCGGAGAAAGCTGCATC 1350
OY 1252 AAGACACGTCGAAGATTGCCAAGGTACCATGTCTGTCTGTCACACACGCTTCCGAG 1311
Db 1351 AAGACACGTCGAAGATTGCCAAGGTACCATGTCTGTCTGTCACACACGCTTCCGAG 1410
OY 1312 GCTCTGTGA 1320
Db 1411 GCTCTGTGA 1419
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RESULT 12

US-10-101-510-715
; Sequence 715, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: MAN, JACKSON
; APPLICANT: MANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101.510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 715
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-715

Query Match 95.2%; Score 1256.2; DB 7; Length 2135;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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OY 52 ACTGACCTTCGGGAAGTCCCTTCCAGAGAAAGATGCTGCGGGAGACACCCCGAGCTA 111
Db 242 ACTTCCTTAGGGGAAGTCCCTTCCAGAGAAAGATGCTGCGGGAGACACCCCGAGCTA 301
OY 112 GTCCAGAGACACAGGTGAACATTAAGAAATTTTCAACAAGTCTCTCGCTTCAAG 171
Db 302 GTCCAGAGACACAGGTGAACATTAAGAAATTTTCAACAAGTCTCTCGCTTCAAG 361
OY 172 GAGAAATGAGAGAAATCATCCAGTGTGGGAGAACTTTCATGAGACATAGAGTGTTCATGTC 231
Db 362 GAGAAATGAGAGAAATCATCCAGTGTGGGAGAACTTTCATGAGACATAGAGTGTTCATGTC 421
OY 232 CTGAACCCCGACGACAGCTGGCCATTTGCAATGCTCTGCTCCCTCAAGCTGGGACCTTCAAG 291
Db 422 CTGAACCCCGACGACAGCTGGCCATTTGCAATGCTCTGCTCCCTCAAGCTGGGACCTTCAAG 481
OY 292 GTCTGAGAAACCTCTGGTGTGCTGTGCTCATCTCCATCCGACAGCTTCGCTGACAG 351
Db 482 GTCTGAGAAACCTCTGGTGTGCTGTGCTCATCTCCGACAGCTTCGCTGACAG 541
OY 352 CCTTCCTACCACTTCATCGGCAAGCTGGCGGTGGAGACCTTCGAGAGTGTCAATTTT 411
Db 542 CCTTCCTACCACTTCATCGGCAAGCTGGCGGTGGAGACCTTCGAGAGTGTCAATTTT 601
OY 412 GTCTACAGCTTCATTTGACTTCCAGCTGTTCCACCGCAAAATAGACCGCACTGTTCTG 471
Db 602 GTCTACAGCTTCATTTGACTTCCAGCTGTTCCACCGCAAAATAGACCGCACTGTTCTG 661
OY 472 TTCAAACTGGGTGGGGGTCAAGGCTCTTCACTGCGCTCGGGAGAGCTGTTCTTCA 531
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Db 662 TTCAAACTGGGTGGGTGCAAGGCTCTTCACTGCTCCGTGGGAGCCTGTTCTCAACA 721
Qy 532 GCCATGCAAGGTAATATTCATTTACAGAGCCCTGGCTATTAAGAAATGTCACAG 591
Db 722 GCCATGCAAGGTAATATTCATTTACAGAGCCCTGGCTATTAAGAAATGTCACAG 781
Qy 592 CCCAAGGCGGTGAGCGTTTGGCCGATGAGGACATGAGCCATTGTATGCGCGTGG 651
Db 782 CCCAAGGCGGTGAGCGTTTGGCCGATGAGGACATGAGCCATTGTATGCGCGTGG 841
Qy 652 CCTCTCTGGGCTGGAAGTGGAGAAATGCAATCTGTTGCTCAGACATTTTCCACAC 711
Db 842 CCTCTCTGGGCTGGAAGTGGAGAAATGCAATCTGTTGCTCAGACATTTTCCACAC 901
Qy 712 ATTTGATGAACCTAATCTGATGTTCTGAGATGCGGGTCAACAAGGTAATCTGTTGATC 771
Db 902 ATTTGATGAACCTAATCTGATGTTCTGAGATGCGGGTCAACAAGGTAATCTGTTGATC 961
Qy 772 GTGTATGCGTATGATATTTCTCTGGAAGGCTCAAGCAGCCGCTCCGATGATTCAG 831
Db 962 GTGTATGCGTATGATATTTCTCTGGAAGGCTCAAGCAGCCGCTCCGATGATTCAG 1021
Qy 832 CGTGGACCCGAGAGAGCATCATTCACAGCTCTGAGATGGAAGGTAAGAGTGAC 891
Db 1022 CGTGGACCCGAGAGAGCATCATTCACAGCTCTGAGATGGAAGGTAAGAGTGAC 1081
Qy 892 CGGCGACCAAGCCCGCATGAGCATTTAGGTTAGCCAGACCTGTGCTGATCTGTG 951
Db 1082 CGGCGACCAAGCCCGCATGAGCATTTAGGTTAGCCAGACCTGTGCTGATCTGTG 1141
Qy 952 GTGTATGATCATGCTGGGCGCTGCTGCTGGAATCAATGATGATGATGATGATG 1011
Db 1142 GTGTATGATCATGCTGGGCGCTGCTGCTGGAATCAATGATGATGATGATGATG 1201
Qy 1012 ATGAACAAGCTATTAAAGAGGTTGTTGATTTCTGAGATGCTCTGCTGGAATCTC 1071
Db 1202 ATGAACAAGCTATTAAAGAGGTTGTTGATTTCTGAGATGCTCTGCTGGAATCTC 1261
Qy 1072 ACCGTGAACCCCATCATCTATGCTCTGAGAGATGAAGACCTGCGACACGCTTTCGGAGC 1131
Db 1262 ACCGTGAACCCCATCATCTATGCTCTGAGAGATGAAGACCTGCGACACGCTTTCGGAGC 1321
Qy 1132 ATGTTTCCCTCTTGAAGGCACTGCGACCTCTGGAATTAAGATGAGGAGACTCCGAGC 1191
Db 1322 ATGTTTCCCTCTTGAAGGCACTGCGACCTCTGGAATTAAGATGAGGAGACTCCGAGC 1381
Qy 1192 TGCCCTGCAAAACAGCAAAACATGCAAGCAGTGTTCACAGAGGCGCAGAAAGCTGCATC 1251
Db 1382 TGCCCTGCAAAACAGCAAAACATGCAAGCAGTGTTCACAGAGGCGCAGAAAGCTGCATC 1441
Qy 1252 AAGAGCAGGTCAAGATTGCGCAAGGTAAACATGTCGTGTTCACAGACAGCTGTCCGAG 1311
Db 1442 AAGAGCAGGTCAAGATTGCGCAAGGTAAACATGTCGTGTTCACAGACAGCTGTCCGAG 1501
Qy 1312 GCTCTGTGA 1320
Db 1502 GCTCTGTGA 1510

RESULT 13
US-10-305-720-1450
; Sequence 1450, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Selthamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
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; SOFTWARE: PERL Program
; SEQ ID NO 1450
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g736236
US-10-305-720-1450

Query Match          95.2%; Score 1256.2; DB 7; Length 2135;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 52 ACTGACCTCTGAGGAATGTCCTTCCAGAGAAAGATGACTGCGGAGACACCCCACTA 111
Db 242 ACTTCCTTTAGGGGAGATGCCCTTCCAGAGAAAGATGACTGCGGAGACACCCCACTA 301
Qy 112 GTCCAGAGACCAAGTGAACAATTACAGAAATTTTACAAAGTCTCTGCTCCCTTCAAG 171
Db 302 GTCCAGAGACCAAGTGAACAATTACAGAAATTTTACAAAGTCTCTGCTCCCTTCAAG 361
Qy 172 GAGAAATGAGAGAAATCATCATGTTGGGAGAACTTCATGACATAGAGTTTCAATGTC 231
Db 362 GAGAAATGAGAGAAATCATCATGTTGGGAGAACTTCATGACATAGAGTTTCAATGTC 421
Qy 232 CTGAACCCCGACGACGCTGGCCATTTGCAATGCTCTGCTCCACGCTGCGGACCTTCAAG 291
Db 422 CTGAACCCCGACGACGCTGGCCATTTGCAATGCTCTGCTCCACGCTGCGGACCTTCAAG 481
Qy 292 GTTCCTGAGAAACCTCTGCTGCTGCGTCAATCCCTCCACCTCCGAGCCTCCGTCAGG 351
Db 482 GTTCCTGAGAAACCTCTGCTGCTGCGTCAATCCCTCCACCTCCGAGCCTCCGTCAGG 541
Qy 352 CTTTCTCAACAATTTCATGCGAGCCTGCGGCTGAGACCTCTCTGAGAGATGTCATTTT 411
Db 542 CTTTCTCAACAATTTCATGCGAGCCTGCGGCTGAGACCTCTCTGAGAGATGTCATTTT 601
Qy 412 GTCTAAGCTTCATTTGACTTCCACGTTTCCACGCGAAAGATAGCGCGAGTGTTCG 471
Db 602 GTCTAAGCTTCATTTGACTTCCACGTTTCCACGCGAAAGATAGCGCGAGTGTTCG 661
Qy 472 TTCAAACTGGGTTGGGTTGACAGGCTCTTCACTGCTCCGTTGGGAGAGCTGTTCTTCA 531
Db 662 TTCAAACTGGGTTGGGTTGACAGGCTCTTCACTGCTCCGTTGGGAGAGCTGTTCTTCA 721
Qy 532 GCCATGCAAGGTAATATTCATTTACAGAGCCCTGGCTATTAAGAAATGTCACAG 591
Db 722 GCCATGCAAGGTAATATTCATTTACAGAGCCCTGGCTATTAAGAAATGTCACAG 781
Qy 592 CCCAAGGCGGTGAGCGTTTGGCCGATGAGGACATGAGCCATTGTATGCGCGTGG 651
Db 782 CCCAAGGCGGTGAGCGTTTGGCCGATGAGGACATGAGCCATTGTATGCGCGTGG 841
Qy 652 CCTCTCTGGGCTGGAAGTGGAGAAATGCAATCTGTTGCTCAGACATTTTCCACAC 711
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Qy 712 ATTTGATGAACCTAATCTGATGTTCTGAGATGCGGGTCAACAAGGTAATCTGTTGATC 771
Db 902 ATTTGATGAACCTAATCTGATGTTCTGAGATGCGGGTCAACAAGGTAATCTGTTGATC 961
Qy 772 GTGTATGCGTATGATATTTCTCTGGAAGGCTCAAGCAGCCGCTCCGATGATTCAG 831
Db 962 GTGTATGCGTATGATATTTCTCTGGAAGGCTCAAGCAGCCGCTCCGATGATTCAG 1021
Qy 832 CGTGGACCCGAGAGAGCATCATTCACAGCTCTGAGATGGAAGGTAAGAGTGAC 891
Db 1022 CGTGGACCCGAGAGAGCATCATTCACAGCTCTGAGATGGAAGGTAAGAGTGAC 1081
Qy 892 CGGCGACCAAGCCCGCATGAGCATTTAGGTTAGCCAGACCTGTGCTGATCTGTG 951
Db 1082 CGGCGACCAAGCCCGCATGAGCATTTAGGTTAGCCAGACCTGTGCTGATCTGTG 1141
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QY 1012 ATGACAAGCTCATTAAGACGGGTTTGAATTGTCAGTATGCTGCTGCTGAATCC 1071
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Db 1202 ATGAACAAGCTCATTAAGACGGGTTTGAATTGTCAGTATGCTGCTGCTGAATCC 1261
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QY 1072 ACCGTAAACCCATCATATGCTCTGAGAGTAAGAACCTGCGACACGCTTCCGAGC 1131
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Db 1262 ACCGTAAACCCATCATATGCTCTGAGAGTAAGAACCTGCGACACGCTTCCGAGC 1321
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QY 1132 ATGTTTCCCTTTTGAAGGCACTGCGACGCTCTGATTAACGATGAGGAACTCGAC 1191
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Db 1322 ATGTTTCCCTTTTGAAGGCACTGCGACGCTCTGATTAACGATGAGGAACTCGAC 1381
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QY 1192 TGGCTGCAAAACAGCCAAACATGACGCCAGTTTCAAGGGCCGCAAAAGCTGATC 1251
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Db 1382 TGGCTGCAAAACAGCCAAACATGACGCCAGTTTCAAGGGCCGCAAAAGCTGATC 1441
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QY 1252 AAGAGCAGGTCMAAGATTGCGCAAGTAAACATGCTGTGTCCACAGACAGCTGCGAG 1311
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Db 1442 AAGAGCAGGTCMAAGATTGCGCAAGTAAACATGCTGTGTCCACAGACAGCTGCGAG 1501
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QY 1312 GCTGTGTGA 1320
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Db 1502 GCTGTGTGA 1510
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RESULT 15

US-10-101-510-409
; Sequence 409, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WAN, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 409
; LENGTH: 5651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-409

Query Match 95.2%; Score 1256.2; DB 7; Length 5651;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 52 ACTGACCTCTGGAAGTCCTTCCAAAGAAAGATGATGCGGAGACAAACCCAGCTA 111
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|
|
Db 260 ACTTCTTTAAGGGAAGTCCCTTCCAAAGAAAGATGATGCGGAGACAAACCCAGCTA 319
|
|
|
QY 112 GTTCCAGCAGACAGGTGAACATTACAGAAATTTTACAAAGATCTTCTGTCTTCAAG 171
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|
|
Db 320 GTTCCAGCAGACAGGTGAACATTACAGAAATTTTACAAAGATCTTCTGTCTTCAAG 379
|
|
|
QY 172 GAGAAATGAGGAACATCCAGTGTGGGAGAACTTCATGACATAGAGTTTCAATGTC 231
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Db 380 GAGAAATGAGGAACATCCAGTGTGGGAGAACTTCATGACATAGAGTTTCAATGTC 439
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|
QY 232 CTGAACCCAGCAGAGCTGACATTTGAGTCTGTCTCTTCAAGCTGAGGACCTTCAAG 291
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